



<110> APPLICANT: GLYCOFI, INC.
 <120> TITLE OF INVENTION: METHODS TO ENGINEER MAMMALIAN-TYPE CARBOHYDRATE
 STRUCTURES
 <130> FILE REFERENCE: GFI/102 PCT
 <140> CURRENT APPLICATION NUMBER: US/10/500,240
 <141> CURRENT FILING DATE: 2004-06-25
 <150> PRIOR APPLICATION NUMBER: 60/344,169
 <151> PRIOR FILING DATE: 2001-12-27
 <160> NUMBER OF SEQ ID NOS: 106
 <170> SOFTWARE: PatentIn Ver. 2.1

<210> SEQ ID NO 1
 <211> LENGTH: 35
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 1
 ggtgttttgt tttctagatc tttgcaytay cartt 35

<210> SEQ ID NO 2
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 2
 agaatttggt gggtaagaat tccarcacca ytcrtg 36

<210> SEQ ID NO 3
 <211> LENGTH: 32
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 3
 cctaagctgg tatgcgttct ctttgccata tc 32

<210> SEQ ID NO 4
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 4
 gcggcataaa caataataga tgctataaag 30

<210> SEQ ID NO 5
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 <400> SEQUENCE: 5
 aattaaccct cactaaaggg 20

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<210> SEQ ID NO 6
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 6
    gtaatacgac tcactatagg gc
22

<210> SEQ ID NO 7
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 7
    ccacatcatc cgtgctacat atag
24

<210> SEQ ID NO 8
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 8
    acgaggcaag ctaaacagat ctcgaagtat cgagggttat ccag
44

<210> SEQ ID NO 9
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 9
    ccatccagtg tcgaaaacga gccaatggtt catgtctata aatc
44

<210> SEQ ID NO 10
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 10
    agcctcagcg ccaacaagcg atgg
24

<210> SEQ ID NO 11
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 11
    ctggataacc ctcgatactt cgagatctgt ttagcttgcc tcgt
44

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<210> SEQ ID NO 12
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 12
      gatttataga catgaaccat tggctcgttt tcgacactgg atgg
                                         44

<210> SEQ ID NO 13
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 13
      atcctttacc gatgctgtat
                                         20

<210> SEQ ID NO 14
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 14
      ataacagtat gtgttacacg cgtgtag
                                         27

<210> SEQ ID NO 15
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 15
      tcctggcgcg ccttcccgag agaactggcc tccctc
                                         36

<210> SEQ ID NO 16
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 16
      aattaattaa ccctagccct ccgctgtatc caacttg
                                         37

<210> SEQ ID NO 17
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 17
      aatgagatga ggctccgcaa tggaactg
                                         28

<210> SEQ ID NO 18

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<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 18
      ctgattgctt atcaacgaga attccttg
28

<210> SEQ ID NO 19
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 19
      tgttggtttc tcagatgatc agttggtg
28

<210> SEQ ID NO 20
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 20
      agagagagat ggctttcttt tctccctgg
29

<210> SEQ ID NO 21
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 21
      aaatcaagtg gatgaaggac atgtggc
27

<210> SEQ ID NO 22
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Primer
<400> SEQUENCE: 22
      agcgatgcta taggcagtct ttgcagag
28

<210> SEQ ID NO 23
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces cerevisiae
<400> SEQUENCE: 23
      His Asp Glu Leu
      1

<210> SEQ ID NO 24
<211> LENGTH: 458
<212> TYPE: PRT

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<213> ORGANISM: Saccharomyces cerevisiae
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (304)..(318)
<223> OTHER INFORMATION: Variable amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (416)..(436)
<223> OTHER INFORMATION: Variable amino acid
<400> SEQUENCE: 24
Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
 1           5           10           15
Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
      20           25           30
Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
      35           40           45
Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Lys Lys
      50           55           60
Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
      65           70           75           80
Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
      85           90           95
Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
      100          105          110
Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
      115          120          125
Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
      130          135          140
Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
      145          150          155          160
Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
      165          170          175
Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
      180          185          190
Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
      195          200          205
Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
      210          215          220
Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
      225          230          235          240
Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
      245          250          255
Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
      260          265          270
His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
      275          280          285
Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe Xaa
      290          295          300
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Val
      305          310          315          320
Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
      325          330          335
Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
      340          345          350
Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg

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		355					360					365							
Ser	Leu	His	Tyr	Gln	Phe	Leu	Ser	Trp	Tyr	His	Trp	Thr	Leu	Pro	Ile				
	370						375					380							
Leu	Ile	Phe	Trp	Ser	Gly	Met	Pro	Phe	Phe	Val	Gly	Pro	Ile	Trp	Tyr				
385					390					395					400				
Val	Leu	His	Glu	Trp	Cys	Trp	Asn	Ser	Tyr	Pro	Pro	Asn	Ser	Gln	Xaa				
			405						410					415					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa				
			420					425					430						
Xaa	Xaa	Xaa	Xaa	Ser	Gly	Ser	Val	Ala	Leu	Ala	Lys	Ser	His	Leu	Arg				
		435				440						445							
Thr	Thr	Ser	Ser	Met	Glu	Lys	Lys	Leu	Asn										
	450					455													

<210> SEQ ID NO 25

<211> LENGTH: 458

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 25

Met	Glu	Gly	Glu	Gln	Ser	Pro	Gln	Gly	Glu	Lys	Ser	Leu	Gln	Arg	Lys				
1				5					10					15					
Gln	Phe	Val	Arg	Pro	Pro	Leu	Asp	Leu	Trp	Gln	Asp	Leu	Lys	Asp	Gly				
			20					25					30						
Val	Arg	Tyr	Val	Ile	Phe	Asp	Cys	Arg	Ala	Asn	Leu	Ile	Val	Met	Pro				
		35				40						45							
Leu	Leu	Ile	Leu	Phe	Glu	Ser	Met	Leu	Cys	Lys	Ile	Ile	Ile	Lys	Lys				
	50					55					60								
Val	Ala	Tyr	Thr	Glu	Ile	Asp	Tyr	Lys	Ala	Tyr	Met	Glu	Gln	Ile	Glu				
65				70						75					80				
Met	Ile	Gln	Leu	Asp	Gly	Met	Leu	Asp	Tyr	Ser	Gln	Val	Ser	Gly	Gly				
			85					90						95					
Thr	Gly	Pro	Leu	Val	Tyr	Pro	Ala	Gly	His	Val	Leu	Ile	Tyr	Lys	Met				
			100					105					110						
Met	Tyr	Trp	Leu	Thr	Glu	Gly	Met	Asp	His	Val	Glu	Arg	Gly	Gln	Val				
		115				120						125							
Phe	Phe	Arg	Tyr	Leu	Tyr	Leu	Leu	Thr	Leu	Ala	Leu	Gln	Met	Ala	Cys				
	130					135					140								
Tyr	Tyr	Leu	Leu	His	Leu	Pro	Pro	Trp	Cys	Val	Val	Leu	Ala	Cys	Leu				
145				150					155					160					
Ser	Lys	Arg	Leu	His	Ser	Ile	Tyr	Val	Leu	Arg	Leu	Phe	Asn	Asp	Cys				
			165					170					175						
Phe	Thr	Thr	Leu	Phe	Met	Val	Val	Thr	Val	Leu	Gly	Ala	Ile	Val	Ala				
			180					185					190						
Ser	Arg	Cys	His	Gln	Arg	Pro	Lys	Leu	Lys	Lys	Ser	Leu	Ala	Leu	Val				
	195					200						205							
Ile	Ser	Ala	Thr	Tyr	Ser	Met	Ala	Val	Ser	Ile	Lys	Met	Asn	Ala	Leu				
	210				215						220								
Leu	Tyr	Phe	Pro	Ala	Met	Met	Ile	Ser	Leu	Phe	Ile	Leu	Asn	Asp	Ala				
225				230					235					240					
Asn	Val	Ile	Leu	Thr	Leu	Leu	Asp	Leu	Val	Ala	Met	Ile	Ala	Trp	Gln				
			245					250					255						
Val	Ala	Val	Ala	Val	Pro	Phe	Leu	Arg	Ser	Phe	Pro	Gln	Gln	Tyr	Leu				
		260				265						270							
His	Cys	Ala	Phe	Asn	Phe	Gly	Arg	Lys	Phe	Met	Tyr	Gln	Trp	Ser	Ile				
	275					280						285							

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Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His
 290          295          300
Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
 305          310          315          320
Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
          325          330          335
Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
          340          345          350
Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
          355          360          365
Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
          370          375          380
Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
 385          390          395          400
Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala
          405          410          415
Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Leu Ala
          420          425          430
Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
          435          440          445
Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
 450          455

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<210> SEQ ID NO 26
<211> LENGTH: 443
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces cerevisiae
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (333)..(347)
<223> OTHER INFORMATION: Variable amino acid
<400> SEQUENCE: 26

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Trp Gln Asp Leu Lys Asp Gly Val Arg Tyr Val Ile Phe Asp Cys Arg
 1          5          10          15
Ala Asn Leu Ile Val Met Pro Leu Leu Ile Leu Phe Glu Ser Met Leu
          20          25          30
Cys Lys Ile Ile Lys Lys Val Ala Tyr Thr Glu Ile Asp Tyr Lys
          35          40          45
Ala Tyr Met Glu Gln Ile Glu Met Ile Gln Leu Asp Gly Met Leu Asp
          50          55          60
Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Gly
          65          70          75          80
His Val Leu Ile Tyr Lys Met Met Tyr Trp Leu Thr Glu Gly Met Asp
          85          90          95
His Val Glu Arg Gly Gln Val Phe Phe Arg Tyr Leu Tyr Leu Leu Thr
          100          105          110
Leu Ala Leu Gln Met Ala Cys Tyr Tyr Leu Leu His Leu Pro Pro Trp
          115          120          125
Cys Val Val Leu Ala Cys Leu Ser Lys Arg Leu His Ser Ile Tyr Val
          130          135          140
Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr Leu Phe Met Val Val Thr
          145          150          155          160
Val Leu Gly Ala Ile Val Ala Ser Arg Cys His Gln Arg Pro Lys Leu
          165          170          175
Lys Lys His Gln Thr Cys Lys Val Pro Pro Phe Val Phe Phe Phe Met

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Trp Gln Glu .

1					5					10					15				
Val	Ala	Ala	Cys	Leu	Cys	Leu	Ala	Glu	Val	Gly	Ile	Thr	Phe	Trp	Val				
			20					25					30						
Ile	His	Arg	Val	Ala	Tyr	Thr	Glu	Ile	Asp	Trp	Lys	Ala	Tyr	Met	Ala				
			35					40					45						
Glu	Val	Glu	Gly	Val	Gly	Thr	Tyr	Asp	Tyr	Thr	Gln	Leu	Gln	Gly	Asp				
			50					55					60						
Thr	Gly	Pro	Leu	Val	Tyr	Pro	Ala	Gly	Phe	Val	Tyr	Ile	Phe	Met	Gly				
			65					70					75						
Leu	Tyr	Tyr	Ala	Thr	Ser	Arg	Gly	Thr	Asp	Ile	Arg	Met	Ala	Gln	Asn				
			85					90					95						
Ile	Phe	Ala	Val	Leu	Tyr	Leu	Ala	Thr	Leu	Leu	Leu	Val	Phe	Leu	Ile				
			100					105					110						
Tyr	His	Gln	Thr	Cys	Lys	Val	Pro	Phe	Val	Phe	Phe	Phe	Met	Cys					
			115					120					125						


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Cys Ala Ser Tyr Arg Val His Ser Ile Phe Val Leu Arg Leu Phe Asn
 130          135          140
Asp Pro Val Ala Met Val Leu Leu Phe Leu Ser Ile Asn Leu Leu Leu
145          150          155          160
Ala Gln Arg Trp Gly Trp Gly Cys Cys Phe Phe Ser Leu Ala Val Ser
          165          170          175
Val Lys Met Asn Val Leu Leu Phe Ala Pro Gly Leu Leu Phe Leu Leu
          180          185          190
Leu Thr Gln Phe Gly Phe Arg Gly Ala Leu Pro Lys Leu Gly Ile Cys
          195          200          205
Ala Gly Leu Gln Val Val Leu Gly Leu Pro Phe Leu Leu Glu Asn Pro
          210          215          220
Ser Gly Tyr Leu Ser Arg Ser Phe Asp Leu Gly Arg Gln Phe Leu Phe
225          230          235          240
His Trp Thr Val Asn Trp Arg Phe Leu Pro Glu Ala Leu Phe Leu His
          245          250          255
Arg Ala Phe His Leu Ala Leu Leu Thr Ala His Leu Thr Leu Leu Leu
          260          265          270
Leu Phe Ala Leu Cys Arg Trp His Arg Thr Gly Glu Ser Ile Leu Ser
          275          280          285
Leu Leu Arg Asp Pro Ser Lys Arg Lys Val Pro Pro Gln Pro Leu Thr
          290          295          300
Pro Asn Gln Ile Val Ser Thr Leu Phe Thr Ser Asn Phe Ile Gly Ile
305          310          315          320
Cys Phe Ser Arg Ser Leu His Tyr Gln Phe Tyr Val Trp Tyr Phe His
          325          330          335
Thr Leu Pro Tyr Leu Leu Trp Ala Met Pro Ala Arg Trp Leu Thr His
          340          345          350
Leu Leu Arg Leu Leu Val Leu Gly Leu Ile Glu Leu Ser Trp Asn Thr
          355          360          365
Tyr Pro Ser Thr Ser
          370

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<210> SEQ ID NO 28

<211> LENGTH: 269

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 28

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Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
 1          5          10          15
Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
          20          25          30
Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
          35          40          45
Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
          50          55          60
Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
          65          70          75          80
Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
          85          90          95
Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
          100          105          110
Tyr Tyr Leu Leu His Pro Trp Cys Val Val Leu Ala Cys Leu Ser Lys
          115          120          125
Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys Phe Thr

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130						135						140					
Thr	Leu	Phe	Met	Val	Val	Thr	Val	Leu	Gly	Ala	Ile	Val	Ala	Ser	Arg		
145						150				155					160		
Cys	His	Gln	Arg	Pro	Lys	Leu	Lys	Lys	Ser	Leu	Ala	Leu	Val	Ile	Ser		
				165					170					175			
Ala	Thr	Tyr	Ser	Met	Ala	Val	Ser	Ile	Lys	Met	Asn	Ala	Leu	Leu	Tyr		
			180					185					190				
Phe	Pro	Ala	Met	Met	Ile	Ser	Leu	Phe	Ile	Leu	Asn	Asp	Ala	Asn	Val		
		195					200					205					
Ile	Leu	Thr	Leu	Leu	Asp	Leu	Val	Ala	Met	Ile	Ala	Trp	Gln	Val	Ala		
	210				215						220						
Val	Ala	Val	Pro	Phe	Leu	Arg	Ser	Phe	Pro	Gln	Gln	Tyr	Leu	His	Cys		
225					230					235					240		
Ala	Phe	Asn	Phe	Gly	Arg	Lys	Phe	Met	Tyr	Gln	Trp	Ser	Ile	Asn	Trp		
			245					250						255			
Gln	Met	Met	Asp	Glu	Glu	Ala	Phe	Asn	Asp	Lys	Arg	Phe					
			260					265									

<210> SEQ ID NO 29

<211> LENGTH: 258

<212> TYPE: PRT

<213> ORGANISM: *Drosophila virilis*

<400> SEQUENCE: 29

Ile	Lys	Tyr	Leu	Ala	Phe	Glu	Pro	Ala	Ala	Leu	Pro	Ile	Val	Ser	Val		
1				5					10					15			
Leu	Ile	Val	Leu	Ala	Glu	Ala	Val	Ile	Asn	Val	Leu	Val	Ile	Gln	Arg		
		20						25					30				
Val	Pro	Tyr	Thr	Glu	Ile	Asp	Trp	Lys	Ala	Tyr	Met	Gln	Glu	Cys	Glu		
		35				40						45					
Gly	Phe	Leu	Asn	Gly	Thr	Thr	Asn	Tyr	Ser	Leu	Leu	Arg	Gly	Asp	Thr		
	50				55					60							
Gly	Pro	Leu	Val	Tyr	Pro	Ala	Ala	Phe	Val	Tyr	Ile	Tyr	Ser	Gly	Leu		
65				70					75					80			
Tyr	Tyr	Leu	Thr	Gly	Gln	Gly	Thr	Asn	Val	Arg	Leu	Ala	Gln	Tyr	Ile		
			85					90					95				
Phe	Ala	Cys	Ile	Tyr	Leu	Leu	Gln	Met	Cys	Leu	Val	Leu	Arg	Leu	Tyr		
		100					105						110				
Thr	Lys	Ser	Arg	Lys	Val	Pro	Pro	Tyr	Val	Leu	Val	Leu	Ser	Ala	Phe		
	115					120						125					
Thr	Ser	Tyr	Arg	Ile	His	Ser	Ile	Tyr	Val	Leu	Arg	Leu	Phe	Asn	Asp		
	130				135				140								
Pro	Val	Ala	Ile	Leu	Leu	Leu	Tyr	Ala	Ala	Leu	Asn	Leu	Phe	Leu	Asp		
145				150					155					160			
Gln	Arg	Trp	Thr	Leu	Gly	Ser	Ile	Cys	Tyr	Ser	Leu	Ala	Val	Gly	Val		
			165					170					175				
Lys	Met	Asn	Ile	Leu	Leu	Phe	Ala	Pro	Ala	Leu	Leu	Leu	Phe	Tyr	Leu		
		180					185						190				
Ala	Asn	Leu	Gly	Val	Leu	Arg	Thr	Leu	Val	Gln	Leu	Thr	Ile	Cys	Ala		
	195					200						205					
Val	Leu	Gln	Leu	Phe	Ile	Gly	Ala	Pro	Phe	Leu	Arg	Thr	His	Pro	Met		
	210				215						220						
Glu	Tyr	Leu	Arg	Gly	Ser	Phe	Asp	Leu	Gly	Arg	Ile	Phe	Glu	His	Lys		
225				230					235					240			
Trp	Thr	Val	Asn	Tyr	Arg	Phe	Leu	Ser	Lys	Glu	Leu	Phe	Glu	Gln	Arg		
			245					250					255				

Glu Phe

<210> SEQ ID NO 30

<211> LENGTH: 267

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 30

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Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro Leu
 1           5           10           15
Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys Val
          20           25           30
Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu Met
          35           40           45
Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly Thr
 50           55           60
Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met Met
 65           70           75           80
Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val Phe
          85           90           95
Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys Tyr
          100          105          110
Tyr Leu Leu His Trp Cys Val Val Leu Ala Cys Leu Ser Lys Arg Leu
          115          120          125
His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr Leu
          130          135          140
Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala Ser Arg Cys His
          145          150          155          160
Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val Ile Ser Ala Thr
          165          170          175
Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu Leu Tyr Phe Pro
          180          185          190
Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala Asn Val Ile Leu
          195          200          205
Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln Val Ala Val Ala
          210          215          220
Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu His Cys Ala Phe
          225          230          235          240
Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile Asn Trp Gln Met
          245          250          255
Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe
          260          265

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<210> SEQ ID NO 31

<211> LENGTH: 257

<212> TYPE: PRT

<213> ORGANISM: *Drosophila melanogaster*

<400> SEQUENCE: 31

```

Lys Tyr Leu Leu Leu Glu Pro Ala Ala Leu Pro Ile Val Gly Leu Phe
 1           5           10           15
Val Leu Leu Ala Glu Leu Val Ile Asn Val Val Val Ile Gln Arg Val
          20           25           30
Pro Tyr Thr Glu Ile Asp Trp Val Ala Tyr Met Gln Glu Cys Glu Gly
          35           40           45
Phe Leu Asn Gly Thr Thr Asn Tyr Ser Leu Leu Arg Gly Asp Thr Gly
          50           55           60

```

Pro Leu Val Tyr Pro Ala Ala Phe Val Tyr Ile Tyr Ser Ala Leu Tyr
 65 70 75 80
 Tyr Val Thr Ser His Gly Thr Asn Val Arg Leu Ala Gln Tyr Ile Phe
 85 90 95
 Ala Gly Ile Tyr Leu Leu Gln Leu Ala Leu Val Leu Arg Leu Tyr Ser
 100 105 110
 Lys Ser Arg Lys Val Pro Pro Tyr Val Leu Val Leu Ser Ala Phe Thr
 115 120 125
 Ser Tyr Arg Ile His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Pro
 130 135 140
 Val Ala Val Leu Leu Leu Tyr Ala Ala Leu Asn Leu Phe Leu Asp Arg
 145 150 155 160
 Arg Trp Thr Leu Gly Ser Thr Phe Phe Ser Leu Ala Val Gly Val Lys
 165 170 175
 Met Asn Ile Leu Leu Phe Ala Pro Ala Leu Leu Leu Phe Tyr Leu Ala
 180 185 190
 Asn Leu Gly Leu Leu Arg Thr Ile Leu Gln Leu Ala Val Cys Gly Val
 195 200 205
 Ile Gln Leu Leu Leu Gly Ala Pro Phe Leu Leu Thr His Pro Val Glu
 210 215 220
 Tyr Leu Arg Gly Ser Phe Asp Leu Gly Arg Ile Phe Glu His Lys Trp
 225 230 235 240
 Thr Val Asn Tyr Arg Phe Leu Ser Arg Asp Val Phe Glu Asn Arg Thr
 245 250 255
 Phe

<210> SEQ ID NO 32

<211> LENGTH: 1377

<212> TYPE: DNA

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 32

atggaagggtg aacagtctcc gcaagggtgaa aagtctctgc aaaggaagca atttgtcaga 60
 cctccgctgg atctgtggca ggatctcaag gacggtgtgc gctacgtgat ctctcattgt 120
 agggccaatc ttatcggtat gccccttttg attttggttcg aaagcatgct gtgcaagatt 180
 atcattaaga aggtagctta cacagagatc gattacaagg cgtacatgga gcagatcgag 240
 atgattcagc tcgatggcat gctggactac tctcagggtga gtggtggaac gggcccgctg 300
 gtgtatccag caggccacgt cttgatctac aagatgatgt actggctaac agagggaatg 360
 gaccacgttg agcgcgggca agtggttttc agatacttgt atctccttac actggcggtta 420
 caaatggcgt gttactacct ttacatctta ccaccgtggg gtgtgggtctt ggcgtgcctc 480
 tctaaaagat tgcactctat ttacgtgcta cggttattca atgattgctt cactactttg 540
 tttatggtcg tcacggtttt gggggctatc gtggccagca ggtgccatca gcgccccaaa 600
 ttaaagaagt cccttgcgct ggtgatctcc gcaacatata gtatggctgt gagcattaag 660
 atgaatgcgc tgttgatatt ccctgcaatg atgatttctc tattcatcct taatgacgcg 720
 aacgtaatcc ttactttggt ggatctcgtt gcgatgattg catggcaagt cgcagttgca 780
 gtgcccttcc tgcgcagctt tccgcaacag tacctgcatt gcgcttttaa tttcggcagg 840
 aagtttatgt accaatggag tatcaattgg caaatgatgg atgaagaggc tttcaatgat 900
 aagagggtcc acttgccctt tttaatcagc cacctgatag cgctcaccac actgttcgtc 960
 acaagatacc ctgcgcatct gcccgattta tgggtcttccc tgtgccatcc gctgaggaaa
 1020
 aatgcagtgc tcaatgccaa tcccgccaag actattccat tcgtttctaat cgcattccaa
 1080
 ttcattcggcg tcctattttc aagggtccctc cactaccagt ttctatcctg gtatcactgg
 1140
 actttgccta tactgatctt ttgggtcgga atgcccttct tcgttggtcc catttggtac
 1200

1260 gtcttgacag agtggtgctg gaattcctat ccaccaaact cacaagcaag cacgctattg
 1320 ttggcattga atactgttct gttgcttcta ttggccttga cgcagctatc tggttcggtc
 1377 gccctcgcca aaagccatct tcgtaccacc agctctatgg aaaaaaagct caactga

<210> SEQ ID NO 33

<211> LENGTH: 458

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 33

Met	Glu	Gly	Glu	Gln	Ser	Pro	Gln	Gly	Glu	Lys	Ser	Leu	Gln	Arg	Lys
1				5					10					15	
Gln	Phe	Val	Arg	Pro	Pro	Leu	Asp	Leu	Trp	Gln	Asp	Leu	Lys	Asp	Gly
			20					25					30		
Val	Arg	Tyr	Val	Ile	Phe	Asp	Cys	Arg	Ala	Asn	Leu	Ile	Val	Met	Pro
		35					40					45			
Leu	Leu	Ile	Leu	Phe	Glu	Ser	Met	Leu	Cys	Lys	Ile	Ile	Ile	Lys	Lys
	50					55					60				
Val	Ala	Tyr	Thr	Glu	Ile	Asp	Tyr	Lys	Ala	Tyr	Met	Glu	Gln	Ile	Glu
65					70					75				80	
Met	Ile	Gln	Leu	Asp	Gly	Met	Leu	Asp	Tyr	Ser	Gln	Val	Ser	Gly	Gly
				85					90					95	
Thr	Gly	Pro	Leu	Val	Tyr	Pro	Ala	Gly	His	Val	Leu	Ile	Tyr	Lys	Met
			100					105						110	
Met	Tyr	Trp	Leu	Thr	Glu	Gly	Met	Asp	His	Val	Glu	Arg	Gly	Gln	Val
		115					120					125			
Phe	Phe	Arg	Tyr	Leu	Tyr	Leu	Leu	Thr	Leu	Ala	Leu	Gln	Met	Ala	Cys
	130					135					140				
Tyr	Tyr	Leu	Leu	His	Leu	Pro	Pro	Trp	Cys	Val	Val	Leu	Ala	Cys	Leu
145					150					155					160
Ser	Lys	Arg	Leu	His	Ser	Ile	Tyr	Val	Leu	Arg	Leu	Phe	Asn	Asp	Cys
				165					170					175	
Phe	Thr	Thr	Leu	Phe	Met	Val	Val	Thr	Val	Leu	Gly	Ala	Ile	Val	Ala
			180					185					190		
Ser	Arg	Cys	His	Gln	Arg	Pro	Lys	Leu	Lys	Lys	Ser	Leu	Ala	Leu	Val
		195					200					205			
Ile	Ser	Ala	Thr	Tyr	Ser	Met	Ala	Val	Ser	Ile	Lys	Met	Asn	Ala	Leu
	210					215					220				
Leu	Tyr	Phe	Pro	Ala	Met	Met	Ile	Ser	Leu	Phe	Ile	Leu	Asn	Asp	Ala
225					230					235					240
Asn	Val	Ile	Leu	Thr	Leu	Leu	Asp	Leu	Val	Ala	Met	Ile	Ala	Trp	Gln
				245					250					255	
Val	Ala	Val	Ala	Val	Pro	Phe	Leu	Arg	Ser	Phe	Pro	Gln	Gln	Tyr	Leu
		260						265					270		
His	Cys	Ala	Phe	Asn	Phe	Gly	Arg	Lys	Phe	Met	Tyr	Gln	Trp	Ser	Ile
		275				280						285			
Asn	Trp	Gln	Met	Met	Asp	Glu	Glu	Ala	Phe	Asn	Asp	Lys	Arg	Phe	His
	290					295					300				
Leu	Ala	Leu	Leu	Ile	Ser	His	Leu	Ile	Ala	Leu	Thr	Thr	Leu	Phe	Val
305					310					315					320
Thr	Arg	Tyr	Pro	Arg	Ile	Leu	Pro	Asp	Leu	Trp	Ser	Ser	Leu	Cys	His
				325					330					335	
Pro	Leu	Arg	Lys	Asn	Ala	Val	Leu	Asn	Ala	Asn	Pro	Ala	Lys	Thr	Ile

<400> SEQUENCE: 34

atgcctccga	tagagccagc	tgaaggccca	aagctttacgc	tgaaaaatgt	tatcggtgat	60
ctagtggctc	ttattcaaaa	cgttttattt	aaccagatt	ttagtgtctt	cgttgcacct	120
cttttatggt	tagctgattc	cattgttatc	aagtgatca	ttggcactgt	ttcctacaca	180
gatattgatt	tttcttcata	tatgcaacaa	atctttaaaa	ttcgacaagg	agaattagat	240
tatagcaaca	tatttggtga	caccgggtcca	ttggtttacc	cagccggcca	tgttcatgct	300
tactcagtac	tttcgtggta	cagtgatggt	ggagaagacg	tcagttctct	tcaacaagca	360
tttggttggt	tatacctagg	ttgcttggtta	ctatccatca	gctcctactt	ttctctggc	420
ttagggaaaa	tacctccggt	ttattttggt	ttgttggtag	cgtccaagag	actgcattca	480
atatttgat	tgagactctt	caatgactgt	ttaacaacat	ttttgatgtt	ggcaactata	540
atcatccttc	aacaagcaag	tagctggagg	aaagatggca	caactattcc	attatctgtc	600
cctgatgctg	cagatacgta	cagtttagcc	atctctgtaa	agatgaatgc	gctgctatac	660
ctcccagcat	tcctactact	catatatctc	atttgtgacg	aaaatttgat	taaagccttg	720
gcacctgttc	tagttttgat	attggtgcaa	gtaggagtcg	gttattcgtt	cattttaccg	780
ttgcactatg	atgattcaggc	aaatgaaatt	cgttctgcct	acttttagaca	ggcttttgac	840
tttagtcgcc	aatttcttta	taagtggaag	gttaattggc	gcttttttaga	ccaagaaact	900
ttcaacaatg	tcattctttca	ccagctcctg	tttgctctcc	atattattac	gttagtcttg	960
ttcatcctca	aqttcctctc	tcctaaaaac	attgaaaaac	cqcttgqtaq	attttgtttg	

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1020      gacattttca aattttggaa gccaacctta tctccaacca atattatcaa cgaccagaa
1080      agaagcccag attttgttta caccgtcatg gctactacca acttaatagg ggtgcttttt
1140      gcaagatctt tacactacca gttcctaagc tggtatgcgt tctctttgcc atatctcctt
1200      tacaaggctc gtctgaactt tatagcatct attattgttt atgccgctca cgagtattgc
1260      tggttggttt tcccagctac agaacaaagt tccgcgttgt tggtatctat cttactactt
1320      atcctgattc tcattttttac caacgaacag ttatttcctt ctcaatcggg ccctgcagaa
1380      aaaaagaata cataa
1395

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- 14 -

<211> LENGTH: 464

<212> TYPE: PRT

<213> ORGANISM: *Pichia pastoris*

<400> SEQUENCE: 35

```

Met Pro Pro Ile Glu Pro Ala Glu Arg Pro Lys Leu Thr Leu Lys Asn
 1           5           10           15
Val Ile Gly Asp Leu Val Ala Leu Ile Gln Asn Val Leu Phe Asn Pro
          20           25           30
Asp Phe Ser Val Phe Val Ala Pro Leu Leu Trp Leu Ala Asp Ser Ile
          35           40           45
Val Ile Lys Val Ile Ile Gly Thr Val Ser Tyr Thr Asp Ile Asp Phe
          50           55           60
Ser Ser Tyr Met Gln Gln Ile Phe Lys Ile Arg Gln Gly Glu Leu Asp
          65           70           75           80
Tyr Ser Asn Ile Phe Gly Asp Thr Gly Pro Leu Val Tyr Pro Ala Gly
          85           90           95
His Val His Ala Tyr Ser Val Leu Ser Trp Tyr Ser Asp Gly Glu
          100          105          110
Asp Val Ser Phe Val Gln Gln Ala Phe Gly Trp Leu Tyr Leu Gly Cys
          115          120          125
Leu Leu Leu Ser Ile Ser Ser Tyr Phe Phe Ser Gly Leu Gly Lys Ile
          130          135          140
Pro Pro Val Tyr Phe Val Leu Leu Val Ala Ser Lys Arg Leu His Ser
          145          150          155          160
Ile Phe Val Leu Arg Leu Phe Asn Asp Cys Leu Thr Thr Phe Leu Met
          165          170          175
Leu Ala Thr Ile Ile Leu Gln Gln Ala Ser Ser Trp Arg Lys Asp
          180          185          190
Gly Thr Thr Ile Pro Leu Ser Val Pro Asp Ala Ala Asp Thr Tyr Ser
          195          200          205
Leu Ala Ile Ser Val Lys Met Asn Ala Leu Leu Tyr Leu Pro Ala Phe
          210          215          220
Leu Leu Leu Ile Tyr Leu Ile Cys Asp Glu Asn Leu Ile Lys Ala Leu
          225          230          235          240
Ala Pro Val Leu Val Leu Ile Leu Val Gln Val Gly Val Gly Tyr Ser
          245          250          255
Phe Ile Leu Pro Leu His Tyr Asp Asp Gln Ala Asn Glu Ile Arg Ser
          260          265          270
Ala Tyr Phe Arg Gln Ala Phe Asp Phe Ser Arg Gln Phe Leu Tyr Lys
          275          280          285
Trp Thr Val Asn Trp Arg Phe Leu Ser Gln Glu Thr Phe Asn Asn Val
          290          295          300
His Phe His Gln Leu Leu Phe Ala Leu His Ile Ile Thr Leu Val Leu
          305          310          315          320
Phe Ile Leu Lys Phe Leu Ser Pro Lys Asn Ile Gly Lys Pro Leu Gly
          325          330          335
Arg Phe Val Leu Asp Ile Phe Lys Phe Trp Lys Pro Thr Leu Ser Pro
          340          345          350
Thr Asn Ile Ile Asn Asp Pro Glu Arg Ser Pro Asp Phe Val Tyr Thr
          355          360          365
Val Met Ala Thr Thr Asn Leu Ile Gly Val Leu Phe Ala Arg Ser Leu
          370          375          380
His Tyr Gln Phe Leu Ser Trp Tyr Ala Phe Ser Leu Pro Tyr Leu Leu
          385          390          395          400
Tyr Lys Ala Arg Leu Asn Phe Ile Ala Ser Ile Ile Val Tyr Ala Ala

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				405					410					415			
His	Glu	Tyr	Cys	Trp	Leu	Val	Phe	Pro	Ala	Thr	Glu	Gln	Ser	Ser	Ala		
			420					425					430				
Leu	Leu	Val	Ser	Ile	Leu	Leu	Leu	Ile	Leu	Ile	Leu	Ile	Phe	Thr	Asn		
		435					440					445					
Glu	Gln	Leu	Phe	Pro	Ser	Gln	Ser	Val	Pro	Ala	Glu	Lys	Lys	Asn	Thr		
	450					455					460						

<210> SEQ ID NO 36
 <211> LENGTH: 418
 <212> TYPE: PRT
 <213> ORGANISM: *Pichia pastoris*
 <220> FEATURE:
 <221> NAME/KEY: MOD_RES
 <222> LOCATION: (209)..(223)
 <223> OTHER INFORMATION: Variable amino acid
 <220> FEATURE:
 <221> NAME/KEY: MOD_RES
 <222> LOCATION: (235)..(246)
 <223> OTHER INFORMATION: Variable amino acid
 <400> SEQUENCE: 36

Arg	Pro	Lys	Leu	Thr	Leu	Lys	Asn	Val	Ile	Gly	Asp	Leu	Val	Ala	Leu		
1				5					10					15			
Ile	Gln	Asn	Val	Leu	Phe	Asn	Pro	Asp	Phe	Ser	Val	Phe	Val	Ala	Pro		
		20					25					30					
Leu	Leu	Trp	Leu	Ala	Asp	Ser	Ile	Val	Ile	Lys	Val	Ile	Ile	Gly	Thr		
		35					40					45					
Val	Ser	Tyr	Thr	Asp	Ile	Asp	Phe	Ser	Ser	Tyr	Met	Gln	Gln	Ile	Phe		
	50					55				60							
Lys	Ile	Arg	Gln	Gly	Glu	Leu	Asp	Tyr	Ser	Asn	Ile	Phe	Gly	Asp	Thr		
	65				70					75				80			
Gly	Pro	Leu	Val	Tyr	Pro	Ala	Gly	His	Val	His	Ala	Tyr	Ser	Val	Leu		
			85					90						95			
Ser	Trp	Tyr	Ser	Asp	Gly	Gly	Glu	Asp	Val	Ser	Phe	Val	Gln	Gln	Ala		
		100					105						110				
Phe	Gly	Trp	Leu	Tyr	Leu	Gly	Cys	Leu	Leu	Leu	Ser	Ile	Ser	Ser	Tyr		
		115				120						125					
Phe	Phe	Ser	Gly	Leu	Gly	Lys	Ile	Pro	Pro	Val	Tyr	Phe	Val	Leu	Leu		
	130					135					140						
Val	Ala	Ser	Lys	Arg	Leu	His	Ser	Ile	Phe	Val	Leu	Arg	Leu	Phe	Asn		
				150						155					160		
Asp	Cys	Leu	Thr	Thr	Phe	Leu	Met	Leu	Ala	Thr	Ile	Ile	Ile	Leu	Gln		
			165						170					175			
Gln	Ala	Ser	Ser	Trp	Arg	Lys	Asp	Gly	Thr	Thr	Ile	Pro	Leu	Ser	Val		
		180						185					190				
Pro	Asp	Ala	Ala	Asp	Thr	Tyr	Ser	Leu	Ala	Ile	Ser	Val	Lys	Met	Asn		
		195					200					205					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys		
	210					215					220						
Asp	Glu	Asn	Leu	Ile	Lys	Ala	Leu	Ala	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa		
	225				230				235					240			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Ser	Phe	Ile	Leu	Pro	Leu	His	Tyr	Asp		
			245					250						255			
Asp	Gln	Ala	Asn	Glu	Ile	Arg	Ser	Ala	Tyr	Phe	Arg	Gln	Ala	Phe	Asp		
		260						265					270				


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Phe Ser Arg Gln Phe Leu Tyr Lys Trp Thr Val Asn Trp Arg Phe Leu
      275                280                285
Ser Gln Glu Thr Phe Asn Asn Val His Phe His Gln Leu Leu Phe Ala
      290                295                300
Leu His Ile Ile Thr Leu Val Leu Phe Ile Leu Lys Phe Leu Ser Pro
      305                310                315                320
Lys Asn Ile Gly Lys Pro Leu Gly Arg Phe Val Leu Asp Ile Phe Lys
      325                330                335
Phe Trp Lys Pro Thr Leu Ser Pro Thr Asn Ile Ile Asn Pro Asp Phe
      340                345                350
Val Tyr Thr Val Met Ala Thr Thr Asn Leu Ile Gly Val Leu Phe Ala
      355                360                365
Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr Ala Phe Ser Leu Pro
      370                375                380
Tyr Leu Leu Tyr Lys Ala Arg Leu Asn Phe Ile Ala Ser Ile Ile Val
      385                390                395                400
Tyr Ala Ala His Glu Tyr Cys Trp Leu Val Phe Pro Ala Thr Glu Gln
      405                410                415
Ser Ser

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<210> SEQ ID NO 37

<211> LENGTH: 398

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 37

```

Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly Val Arg Tyr
  1          5          10          15
Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro Leu Leu Ile
      20          25          30
Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys Val Ala Tyr
      35          40          45
Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu Met Ile Gln
      50          55          60
Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro
      65          70          75          80
Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met Met Tyr Trp
      85          90          95
Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val Phe Phe Arg
      100         105         110
Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys Tyr Tyr Leu
      115         120         125
Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu Ser Lys Arg
      130         135         140
Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr
      145         150         155         160
Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala Ser Arg Cys
      165         170         175
His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val Ile Ser Ala
      180         185         190
Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu Leu Tyr Phe
      195         200         205
Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala Asn Val Ile
      210         215         220
Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln Val Ala Val
      225         230         235         240

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Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu His Cys Ala
      245                      250                      255
Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile Asn Trp Gln
      260                      265                      270
Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His Leu Ala Leu
      275                      280                      285
Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val Thr Arg Tyr
      290                      295                      300
Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His Pro Leu Arg
305                      310                      315                      320
Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile Pro Phe Val
      325                      330                      335
Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg Ser Leu His
      340                      345                      350
Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile Leu Ile Phe
      355                      360                      365
Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr Val Leu His
      370                      375                      380
Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala Ser
385                      390                      395

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<210> SEQ ID NO 38
<211> LENGTH: 387
<212> TYPE: PRT
<213> ORGANISM: Pichia pastoris
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (183)..(197)
<223> OTHER INFORMATION: Variable amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (209)..(220)
<223> OTHER INFORMATION: Variable amino acid
<400> SEQUENCE: 38

```

```

Ser Val Phe Val Ala Pro Leu Leu Trp Leu Ala Asp Ser Ile Val Ile
 1           5           10           15
Lys Val Ile Ile Gly Thr Val Ser Tyr Thr Asp Ile Asp Phe Ser Ser
      20           25           30
Tyr Met Gln Gln Ile Phe Lys Ile Arg Gln Gly Glu Leu Asp Tyr Ser
      35           40           45
Asn Ile Phe Gly Asp Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val
      50           55           60
His Ala Tyr Ser Val Leu Ser Trp Tyr Ser Asp Gly Gly Glu Asp Val
      65           70           75           80
Ser Phe Val Gln Gln Ala Phe Gly Trp Leu Tyr Leu Gly Cys Leu Leu
      85           90           95
Leu Ser Ile Ser Ser Tyr Phe Phe Ser Gly Leu Gly Lys Ile Pro Pro
      100          105          110
Val Tyr Phe Val Leu Leu Val Ala Ser Lys Arg Leu His Ser Ile Phe
      115          120          125
Val Leu Arg Leu Phe Asn Asp Cys Leu Thr Thr Phe Leu Met Leu Ala
      130          135          140
Thr Ile Ile Ile Leu Gln Ala Ser Ser Trp Arg Lys Asp Gly Thr
      145          150          155          160
Thr Ile Pro Leu Ser Val Pro Asp Ala Ala Asp Thr Tyr Ser Leu Ala

```

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      165      170      175
Ile Ser Val Lys Met Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      180      185      190
Xaa Xaa Xaa Xaa Xaa Cys Asp Glu Asn Leu Ile Lys Ala Leu Ala Pro
      195      200      205
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Ser Phe Ile
      210      215      220
Leu Pro Leu His Tyr Asp Asp Gln Ala Asn Glu Ile Arg Ser Ala Tyr
225      230      235      240
Phe Arg Gln Ala Phe Asp Phe Ser Arg Gln Phe Leu Tyr Lys Trp Thr
      245      250      255
Val Asn Trp Arg Phe Leu Ser Gln Glu Thr Phe Asn Asn Val His Phe
      260      265      270
His Gln Leu Leu Phe Ala Leu His Ile Ile Thr Leu Val Leu Phe Ile
      275      280      285
Pro Leu Gly Arg Phe Val Leu Asp Ile Phe Lys Phe Trp Lys Pro Thr
      290      295      300
Leu Ser Pro Thr Asn Ile Asn Asp Pro Glu Arg Ser Pro Asp Phe
305      310      315      320
Val Tyr Thr Val Met Ala Thr Thr Asn Leu Ile Gly Val Leu Phe Ala
      325      330      335
Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr Ala Phe Ser Leu Pro
      340      345      350
Tyr Leu Leu Tyr Lys Ala Arg Leu Asn Phe Ile Ala Ser Ile Ile Val
      355      360      365
Tyr Ala Ala His Glu Tyr Cys Trp Leu Val Phe Pro Ala Thr Glu Gln
      370      375      380
Ser Ser Ala
385

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<210> SEQ ID NO 39
<211> LENGTH: 373
<212> TYPE: PRT
<213> ORGANISM: Neurospora crassa
<400> SEQUENCE: 39

```

```

Ser Lys Leu Ile Pro Pro Ala Leu Phe Leu Val Asp Ala Leu Leu Cys
 1      5      10      15
Gly Leu Ile Ile Trp Lys Val Pro Tyr Thr Glu Ile Asp Trp Ala Ala
      20      25      30
Tyr Met Glu Gln Val Ser Gln Ile Leu Ser Gly Glu Arg Asp Tyr Thr
      35      40      45
Lys Val Arg Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Ala His Val
      50      55      60
Tyr Ile Tyr Thr Gly Leu Tyr His Leu Thr Asp Glu Gly Arg Asn Ile
      65      70      75      80
Leu Leu Ala Gln Gln Leu Phe Ala Gly Leu Tyr Met Val Thr Leu Ala
      85      90      95
Val Val Met Gly Cys Tyr Trp Gln Ala Lys Ala Pro Pro Tyr Leu Phe
      100      105      110
Pro Leu Leu Thr Leu Ser Lys Arg Leu His Ser Ile Phe Val Leu Arg
      115      120      125
Cys Phe Asn Asp Cys Phe Ala Val Leu Phe Leu Trp Leu Ala Ile Phe
      130      135      140
Phe Phe Gln Arg Arg Asn Trp Gln Ala Gly Ala Leu Leu Tyr Thr Leu
145      150      155      160

```

```

Gly Leu Gly Val Lys Met Thr Leu Leu Leu Ser Leu Pro Ala Val Gly
      165      170      175
Ile Val Leu Phe Leu Gly Ser Gly Ser Phe Val Thr Thr Leu Gln Leu
      180      185      190
Val Ala Thr Met Gly Leu Val Gln Ile Leu Ile Gly Val Pro Phe Leu
      195      200      205
Ala His Tyr Pro Thr Glu Tyr Leu Ser Arg Ala Phe Glu Leu Ser Arg
      210      215      220
Gln Phe Phe Phe Lys Trp Thr Val Asn Trp Arg Phe Val Gly Glu Glu
225      230      235      240
Ile Phe Leu Ser Lys Gly Phe Ala Leu Thr Leu Leu Ala Leu His Val
      245      250      255
Leu Val Leu Gly Ile Phe Ile Thr Thr Arg Trp Ile Lys Pro Ala Arg
      260      265      270
Lys Ser Leu Val Gln Leu Ile Ser Pro Val Leu Leu Ala Gly Lys Pro
      275      280      285
Pro Leu Thr Val Pro Glu His Arg Ala Ala Ala Arg Asp Val Thr Pro
      290      295      300
Arg Tyr Ile Met Thr Thr Ile Leu Ser Ala Asn Ala Val Gly Leu Leu
305      310      315      320
Phe Ala Arg Ser Leu His Tyr Gln Phe Tyr Ala Tyr Val Ala Trp Ser
      325      330      335
Thr Pro Phe Leu Leu Trp Arg Ala Gly Leu His Pro Val Leu Val Tyr
      340      345      350
Leu Leu Trp Ala Val His Glu Trp Ala Trp Asn Val Phe Pro Ser Thr
      355      360      365
Pro Ala Ser Ser Ala
      370

```

```

<210> SEQ ID NO 40
<211> LENGTH: 390
<212> TYPE: PRT
<213> ORGANISM: Pichia pastoris
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (176)..(190)
<223> OTHER INFORMATION: Variable amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (202)..(213)
<223> OTHER INFORMATION: Variable amino acid
<400> SEQUENCE: 40

```

```

Leu Trp Leu Ala Asp Ser Ile Val Ile Lys Val Ile Ile Gly Thr Val
 1      5      10      15
Ser Tyr Thr Asp Ile Asp Phe Ser Ser Tyr Met Gln Gln Ile Phe Lys
      20      25      30
Ile Arg Gln Gly Glu Leu Asp Tyr Ser Asn Ile Phe Gly Asp Thr Gly
      35      40      45
Pro Leu Val Tyr Pro Ala Gly His Val His Ala Tyr Ser Val Leu Ser
      50      55      60
Trp Tyr Ser Asp Gly Gly Glu Asp Val Ser Phe Val Gln Gln Ala Phe
      65      70      75      80
Gly Trp Leu Tyr Leu Gly Cys Leu Leu Leu Ser Ile Ser Ser Tyr Phe
      85      90      95
Phe Ser Gly Leu Gly Lys Ile Pro Pro Val Tyr Phe Val Leu Leu Val

```

				100					105				110				
Ala	Ser	Lys	Arg	Leu	His	Ser	Ile	Phe	Val	Leu	Arg	Leu	Phe	Asn	Asp		
		115					120					125					
Cys	Leu	Thr	Thr	Phe	Leu	Met	Leu	Ala	Thr	Ile	Ile	Ile	Leu	Gln	Gln		
	130					135					140						
Ala	Ser	Ser	Trp	Arg	Lys	Asp	Gly	Thr	Thr	Ile	Pro	Leu	Ser	Val	Pro		
145					150					155					160		
Asp	Ala	Ala	Asp	Thr	Tyr	Ser	Leu	Ala	Ile	Ser	Val	Lys	Met	Asn	Xaa		
			165						170					175			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Asp		
			180					185					190				
Glu	Asn	Leu	Ile	Lys	Ala	Leu	Ala	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa		
	195						200					205					
Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Ser	Phe	Ile	Leu	Pro	Leu	His	Tyr	Asp	Asp		
	210				215						220						
Gln	Ala	Asn	Glu	Ile	Arg	Ser	Ala	Tyr	Phe	Arg	Gln	Ala	Phe	Asp	Phe		
225					230					235					240		
Ser	Arg	Gln	Phe	Leu	Tyr	Lys	Trp	Thr	Val	Asn	Trp	Arg	Phe	Leu	Ser		
			245						250					255			
Gln	Glu	Thr	Phe	Asn	Asn	Val	His	Phe	His	Gln	Leu	Leu	Phe	Ala	Leu		
			260					265					270				
His	Ile	Ile	Thr	Leu	Val	Leu	Phe	Ile	Leu	Lys	Phe	Leu	Ser	Pro	Lys		
	275						280					285					
Asn	Ile	Gly	Lys	Pro	Leu	Gly	Arg	Phe	Val	Leu	Asp	Ile	Phe	Lys	Phe		
	290				295					300							
Trp	Lys	Pro	Thr	Leu	Ser	Pro	Thr	Asn	Ile	Ile	Asn	Asp	Pro	Glu	Arg		
305					310				315						320		
Ser	Pro	Asp	Phe	Val	Tyr	Thr	Val	Met	Ala	Thr	Thr	Asn	Leu	Ile	Gly		
			325					330						335			
Val	Leu	Phe	Ala	Arg	Ser	Leu	His	Tyr	Gln	Phe	Leu	Ser	Trp	Tyr	Ala		
			340					345					350				
Phe	Ser	Leu	Pro	Tyr	Leu	Leu	Tyr	Lys	Ala	Arg	Leu	Asn	Phe	Ile	Ala		
	355						360					365					
Ser	Ile	Ile	Val	Tyr	Ala	Ala	His	Glu	Tyr	Cys	Trp	Leu	Val	Phe	Pro		
	370				375						380						
Ala	Thr	Glu	Gln	Ser	Ser												
385					390												

<210> SEQ ID NO 41
 <211> LENGTH: 355
 <212> TYPE: PRT
 <213> ORGANISM: Schizosaccharomyces pombe
 <400> SEQUENCE: 41

Leu	Leu	Leu	Leu	Glu	Ile	Pro	Phe	Val	Phe	Ala	Ile	Ile	Ser	Lys	Val		
1				5					10					15			
Pro	Tyr	Thr	Glu	Ile	Asp	Trp	Ile	Ala	Tyr	Met	Glu	Gln	Val	Asn	Ser		
			20					25					30				
Phe	Leu	Leu	Gly	Glu	Arg	Asp	Tyr	Lys	Ser	Leu	Val	Gly	Cys	Thr	Gly		
			35				40					45					
Pro	Leu	Val	Tyr	Pro	Gly	Gly	His	Val	Phe	Leu	Tyr	Thr	Leu	Leu	Tyr		
	50				55						60						
Tyr	Leu	Thr	Asp	Gly	Gly	Thr	Asn	Ile	Val	Arg	Ala	Gln	Tyr	Ile	Phe		
	65				70					75					80		
Ala	Phe	Val	Tyr	Trp	Ile	Thr	Thr	Ala	Ile	Val	Gly	Tyr	Leu	Phe	Lys		
				85					90					95			

```

Ile Val Arg Ala Pro Phe Tyr Ile Tyr Val Leu Leu Ile Leu Ser Lys
      100      105      110
Arg Leu His Ser Ile Phe Ile Leu Arg Leu Phe Asn Asp Gly Phe Asn
      115      120      125
Ser Leu Phe Ser Ser Leu Phe Ile Leu Ser Ser Cys Lys Lys Lys Trp
      130      135      140
Val Arg Ala Ser Ile Leu Leu Ser Val Ala Cys Ser Val Lys Met Ser
145      150      155      160
Ser Leu Leu Tyr Val Pro Ala Tyr Leu Val Leu Leu Leu Gln Ile Leu
      165      170      175
Gly Pro Lys Lys Thr Trp Met His Ile Phe Val Ile Ile Ile Val Gln
      180      185      190
Ile Leu Phe Ser Ile Pro Phe Leu Ala Tyr Phe Trp Ser Tyr Trp Thr
      195      200      205
Gln Ala Phe Asp Phe Gly Arg Ala Phe Asp Tyr Lys Trp Thr Val Asn
210      215      220
Trp Arg Phe Ile Pro Arg Ser Ile Phe Glu Ser Thr Ser Phe Ser Thr
225      230      235      240
Ser Ile Leu Phe Leu His Val Ala Leu Leu Val Ala Phe Thr Cys Lys
      245      250      255
His Trp Asn Lys Leu Ser Arg Ala Thr Pro Phe Ala Met Val Asn Ser
      260      265      270
Met Leu Thr Leu Lys Pro Leu Pro Lys Leu Gln Leu Ala Thr Pro Asn
      275      280      285
Phe Ile Phe Thr Ala Leu Ala Thr Ser Asn Leu Ile Gly Ile Leu Cys
290      295      300
Ala Arg Ser Leu His Tyr Gln Phe Tyr Ala Trp Phe Ala Trp Tyr Ser
305      310      315      320
Pro Tyr Leu Cys Tyr Gln Ala Ser Phe Pro Ala Pro Ile Val Ile Gly
      325      330      335
Leu Trp Met Leu Gln Glu Tyr Ala Trp Asn Val Phe Pro Ser Thr Lys
      340      345      350
Leu Ser Ser
      355

```

```

<210> SEQ ID NO 42
<211> LENGTH: 390
<212> TYPE: PRT
<213> ORGANISM: Pichia pastoris
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (176)..(190)
<223> OTHER INFORMATION: Variable amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (202)..(213)
<223> OTHER INFORMATION: Variable amino acid
<400> SEQUENCE: 42

```

```

Leu Trp Leu Ala Asp Ser Ile Val Ile Lys Val Ile Ile Gly Thr Val
 1           5           10           15
Ser Tyr Thr Asp Ile Asp Phe Ser Ser Tyr Met Gln Gln Ile Phe Lys
      20           25           30
Ile Arg Gln Gly Glu Leu Asp Tyr Ser Asn Ile Phe Gly Asp Thr Gly
      35           40           45
Pro Leu Val Tyr Pro Ala Gly His Val His Ala Tyr Ser Val Leu Ser

```

50						55						60					
Trp	Tyr	Ser	Asp	Gly	Gly	Glu	Asp	Val	Ser	Phe	Val	Gln	Gln	Ala	Phe		
65					70					75					80		
Gly	Trp	Leu	Tyr	Leu	Gly	Cys	Leu	Leu	Leu	Ser	Ile	Ser	Ser	Tyr	Phe		
				85					90					95			
Phe	Ser	Gly	Leu	Gly	Lys	Ile	Pro	Pro	Val	Tyr	Phe	Val	Leu	Leu	Val		
			100					105					110				
Ala	Ser	Lys	Arg	Leu	His	Ser	Ile	Phe	Val	Leu	Arg	Leu	Phe	Asn	Asp		
		115					120					125					
Cys	Leu	Thr	Thr	Phe	Leu	Met	Leu	Ala	Thr	Ile	Ile	Ile	Leu	Gln	Gln		
	130					135					140						
Ala	Ser	Ser	Trp	Arg	Lys	Asp	Gly	Thr	Thr	Ile	Pro	Leu	Ser	Val	Pro		
145					150					155					160		
Asp	Ala	Ala	Asp	Thr	Tyr	Ser	Leu	Ala	Ile	Ser	Val	Lys	Met	Asn	Xaa		
				165					170					175			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Asp		
			180					185					190				
Glu	Asn	Leu	Ile	Lys	Ala	Leu	Ala	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa		
		195					200					205					
Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Ser	Phe	Ile	Leu	Pro	Leu	His	Tyr	Asp	Asp		
	210				215						220						
Gln	Ala	Asn	Glu	Ile	Arg	Ser	Ala	Tyr	Phe	Arg	Gln	Ala	Phe	Asp	Phe		
225					230					235					240		
Ser	Arg	Gln	Phe	Leu	Tyr	Lys	Trp	Thr	Val	Asn	Trp	Arg	Phe	Leu	Ser		
				245					250				255				
Gln	Glu	Thr	Phe	Asn	Asn	Val	His	Phe	His	Gln	Leu	Leu	Phe	Ala	Leu		
			260					265				270					
His	Ile	Ile	Thr	Leu	Val	Leu	Phe	Ile	Leu	Lys	Phe	Leu	Ser	Pro	Lys		
		275					280					285					
Asn	Ile	Gly	Lys	Pro	Leu	Gly	Arg	Phe	Val	Leu	Asp	Ile	Phe	Lys	Phe		
	290					295					300						
Trp	Lys	Pro	Thr	Leu	Ser	Pro	Thr	Asn	Ile	Ile	Asn	Asp	Pro	Glu	Arg		
305					310					315					320		
Ser	Pro	Asp	Phe	Val	Tyr	Thr	Val	Met	Ala	Thr	Thr	Asn	Leu	Ile	Gly		
			325						330					335			
Val	Leu	Phe	Ala	Arg	Ser	Leu	His	Tyr	Gln	Phe	Leu	Ser	Trp	Tyr	Ala		
			340					345					350				
Phe	Ser	Leu	Pro	Tyr	Leu	Leu	Tyr	Lys	Ala	Arg	Leu	Asn	Phe	Ile	Ala		
		355					360					365					
Ser	Ile	Ile	Val	Tyr	Ala	Ala	His	Glu	Tyr	Cys	Trp	Leu	Val	Phe	Pro		
	370					375					380						
Ala	Thr	Glu	Gln	Ser	Ser												
385					390												

<210> SEQ ID NO 43

<211> LENGTH: 363

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 43

Leu	Ile	Leu	Ala	Asp	Ala	Ile	Leu	Val	Ala	Leu	Ile	Ile	Ala	Tyr	Val		
1				5					10					15			
Pro	Tyr	Thr	Lys	Ile	Asp	Trp	Asp	Ala	Tyr	Met	Ser	Gln	Val	Ser	Gly		
			20					25					30				
Phe	Leu	Gly	Glu	Arg	Asp	Tyr	Gly	Asn	Leu	Lys	Gly	Asp	Thr	Gly			
		35				40						45					

Pro	Leu	Val	Tyr	Pro	Ala	Gly	Phe	Leu	Tyr	Val	Tyr	Ser	Ala	Val	Gln
	50					55					60				
Asn	Leu	Thr	Gly	Gly	Glu	Val	Tyr	Pro	Ala	Gln	Ile	Leu	Phe	Gly	Val
65					70					75					80
Leu	Tyr	Ile	Val	Asn	Leu	Gly	Ile	Val	Leu	Ile	Ile	Tyr	Val	Lys	Thr
				85					90					95	
Asp	Val	Val	Pro	Trp	Trp	Ala	Leu	Ser	Leu	Leu	Cys	Leu	Ser	Lys	Arg
			100					105					110		
Ile	His	Ser	Ile	Phe	Val	Leu	Arg	Leu	Phe	Asn	Asp	Cys	Phe	Ala	Met
	115						120					125			
Thr	Leu	Leu	His	Ala	Ser	Met	Ala	Leu	Phe	Leu	Tyr	Arg	Lys	Trp	His
	130					135					140				
Leu	Gly	Met	Leu	Val	Phe	Ser	Gly	Ala	Val	Ser	Val	Lys	Met	Asn	Val
145					150					155					160
Leu	Leu	Tyr	Ala	Pro	Thr	Leu	Leu	Leu	Leu	Leu	Leu	Lys	Ala	Met	Asn
				165					170					175	
Ile	Ile	Gly	Val	Val	Ser	Ala	Leu	Ala	Gly	Ala	Ala	Leu	Ala	Gln	Ile
			180					185					190		
Leu	Val	Gly	Leu	Pro	Phe	Leu	Ile	Thr	Tyr	Pro	Val	Ser	Tyr	Ile	Ala
	195						200					205			
Asn	Ala	Phe	Asp	Leu	Gly	Arg	Val	Phe	Ile	His	Phe	Trp	Ser	Val	Asn
	210				215						220				
Phe	Lys	Phe	Val	Pro	Glu	Arg	Val	Phe	Val	Ser	Lys	Glu	Phe	Ala	Val
225					230					235					240
Cys	Leu	Leu	Ile	Ala	His	Leu	Phe	Leu	Leu	Val	Ala	Phe	Ala	Asn	Tyr
				245					250					255	
Lys	Trp	Cys	Lys	His	Glu	Gly	Gly	Ile	Ile	Gly	Phe	Met	Arg	Ser	Arg
			260					265					270		
His	Phe	Phe	Leu	Thr	Leu	Pro	Ser	Ser	Leu	Ser	Phe	Ser	Asp	Val	Ser
	275						280					285			
Ala	Ser	Arg	Ile	Ile	Thr	Lys	Glu	His	Val	Val	Thr	Ala	Met	Phe	Val
	290					295					300				
Gly	Asn	Phe	Ile	Gly	Ile	Val	Phe	Ala	Arg	Ser	Leu	His	Tyr	Gln	Phe
305					310					315					320
Tyr	Ser	Trp	Tyr	Phe	Tyr	Ser	Leu	Pro	Tyr	Leu	Leu	Trp	Arg	Thr	Pro
				325					330					335	
Phe	Pro	Thr	Trp	Leu	Arg	Leu	Ile	Met	Phe	Leu	Gly	Ile	Glu	Leu	Cys
			340					345					350		
Trp	Asn	Val	Tyr	Pro	Ser	Thr	Pro	Ser	Ser	Ser					
	355						360								

<210> SEQ ID NO 44

<211> LENGTH: 428

<212> TYPE: DNA

<213> ORGANISM: Kluyveromyces lactis

<400> SEQUENCE: 44

```

tttgtttaca agctgatacc aacgaacatg aatacaccgg caggttttact gaagattggc 60
aaagctaacc ttttacatcc ttttaccgat gctgtattca gtgcgatgag agtaaacgca 120
gaacaaattg catacatttt acttggtacc aattacattg gagtactatt tgctcgatca 180
ttacactacc aattcctatc ttggtaccat tggacgttac cagtactatt gaattgggcc 240
aatgttccgt atccgctatg tgtgctatgg tacctaacac atgagtggtg ctggaacagc 300
tatccgccaa acgctactgc atccacactg ctacacgcgt gtaacacata ctgttattgg 360
ctgtattctt aagaggaccc gcaaactcga aaagtgggtga taacgaaaca acacacgaga 420
aagctgag

```


<210> SEQ ID NO 45

<211> LENGTH: 141

<212> TYPE: PRT

<213> ORGANISM: Kluyveromyces lactis

<400> SEQUENCE: 45

```

Phe Val Tyr Lys Leu Ile Pro Thr Asn Met Asn Thr Pro Ala Gly Leu
 1           5           10           15
Leu Lys Ile Gly Lys Ala Asn Leu Leu His Pro Phe Thr Asp Ala Val
           20           25           30
Phe Ser Ala Met Arg Val Asn Ala Glu Gln Ile Ala Tyr Ile Leu Leu
           35           40           45
Val Thr Asn Tyr Ile Gly Val Leu Phe Ala Arg Ser Leu His Tyr Gln
           50           55           60
Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Val Leu Leu Asn Trp Ala
           65           70           75           80
Asn Val Pro Tyr Pro Leu Cys Val Leu Trp Tyr Leu Thr His Glu Trp
           85           90           95
Cys Trp Asn Ser Tyr Pro Pro Asn Ala Thr Ala Ser Thr Leu Leu His
           100          105          110
Ala Cys Asn Thr Tyr Cys Tyr Trp Leu Tyr Ser Glu Asp Pro Gln Thr
           115          120          125
Arg Lys Val Val Ile Thr Lys Gln His Thr Arg Lys Leu
           130          135          140

```

<210> SEQ ID NO 46

<211> LENGTH: 118

<212> TYPE: PRT

<213> ORGANISM: Kluyveromyces lactis

<400> SEQUENCE: 46

```

Ala Asn Leu Leu His Pro Phe Thr Asp Ala Val Phe Ser Ala Met Arg
 1           5           10           15
Val Asn Ala Glu Gln Ile Ala Tyr Ile Leu Leu Val Thr Asn Tyr Ile
           20           25           30
Gly Val Leu Phe Ala Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr
           35           40           45
His Trp Thr Leu Pro Val Leu Asn Trp Ala Asn Val Pro Tyr Pro
           50           55           60
Leu Cys Val Leu Trp Tyr Leu Thr His Glu Trp Cys Trp Asn Ser Tyr
           65           70           75           80
Pro Pro Asn Ala Thr Ala Ser Thr Leu Leu His Ala Cys Asn Thr Tyr
           85           90           95
Cys Tyr Trp Leu Tyr Ser Glu Asp Pro Gln Thr Arg Lys Val Val Ile
           100          105          110
Thr Lys Gln His Thr Arg
           115

```

<210> SEQ ID NO 47

<211> LENGTH: 117

<212> TYPE: PRT

<213> ORGANISM: Saccharomyces cerevisiae

<400> SEQUENCE: 47

```

Ser Ser Leu Cys His Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn
 1           5           10           15
Pro Ala Lys Thr Ile Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly
           20           25           30

```

```

Val Leu Phe Ser Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His
    35              40              45
Trp Thr Leu Pro Ile Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val
    50              55              60
Gly Pro Ile Trp Tyr Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro
    65              70              75              80
Pro Asn Ser Gln Ala Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu
    85              90              95
Leu Leu Leu Leu Ala Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala
    100              105              110
Lys Ser His Leu Arg
    115

```

<210> SEQ ID NO 48

<211> LENGTH: 113

<212> TYPE: PRT

<213> ORGANISM: Kluyveromyces lactis

<400> SEQUENCE: 48

```

Phe Thr Asp Ala Val Phe Ser Ala Met Arg Val Asn Ala Glu Gln Ile
  1              5              10              15
Ala Tyr Ile Leu Leu Val Thr Asn Tyr Ile Gly Val Leu Phe Ala Arg
    20              25              30
Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Val
    35              40              45
Leu Leu Asn Trp Ala Asn Val Pro Tyr Pro Leu Cys Val Leu Trp Tyr
    50              55              60
Leu Thr His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ala Thr Ala
    65              70              75              80
Ser Thr Leu Leu His Ala Cys Asn Thr Tyr Cys Tyr Trp Leu Tyr Ser
    85              90              95
Glu Asp Pro Gln Thr Arg Lys Val Val Ile Thr Lys Gln His Thr Arg
    100              105              110
Lys

```

<210> SEQ ID NO 49

<211> LENGTH: 106

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 49

```

Phe Ser Asp Val Ser Ala Ser Arg Ile Ile Thr Lys Glu His Val Val
  1              5              10              15
Thr Ala Met Phe Val Gly Asn Phe Ile Gly Ile Val Phe Ala Arg Ser
    20              25              30
Leu His Tyr Gln Phe Tyr Ser Trp Tyr Phe Tyr Ser Leu Pro Tyr Leu
    35              40              45
Leu Trp Arg Thr Pro Phe Pro Thr Trp Leu Arg Leu Ile Met Phe Leu
    50              55              60
Gly Ile Glu Leu Cys Trp Asn Val Tyr Pro Ser Thr Pro Ser Ser Ser
    65              70              75              80
Gly Leu Leu Leu Cys Leu His Leu Ile Ile Leu Val Gly Leu Trp Leu
    85              90              95
Ala Pro Ser Val Asp Pro Tyr Gln Leu Lys
    100              105

```

<210> SEQ ID NO 50

<211> LENGTH: 1668

<212> TYPE: DNA

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 50

```

atgaattgca aggcggtaac cattagttta ttactgttgt tatttttaac aagagtatat 60
attcagccga cattctcgtt aatttcagat tgcgatgaaa cttttaatta ttgggaacca 120
ttaaatttat tgggtacgtg atttggtaaa caaacctggg aatattcacc cgagtattct 180
attagatcat gggctttctt attacctttt tactgtattc tttatccagt aaacaaattt 240
actgacctag aaagtcattg gaactttttc atcacaagag catgcttagg ctttttttagt 300
tttatcatgg aattttaact acatcgtgaa attgcaggca gcttggcatt gcaaatacgca 360
aatatttgga ttattttcca attgtttaat cggggtcgtt tccatgcac tgtggaatta 420
ttgccttctg ccgttgccat gttgttgtat gtaggtgcca ccagacactc tctacgctat 480
ctgtccactg ggtctacttc taacttttacg aaaagtttag cgtacaattt cctggctagt 540
atactaggct ggccatttgt tttaatttta agcttgccat tatgtttaca ttaccttttc 600
aaccatagaa ttatttctac catcagaacc gcattcgact gctgtttgat attttcattg 660
actgcatttg ctgtgattgt cactgacagt atatttttac ggaagcttgc tcctgtatca 720
tggaacatct tattttacaa tgtcattaat gcaagtgagg aatctggccc aaatattttc 780
ggggttgagc catggtacta ctatccacta aatttgttac tgaatttccc actgcctgtg 840
ctagtttttag ctattttggg aattttccat ttgagattat ggccattatg ggcatacatta 900
ttcacatgga ttgccgtttt cactcaacaa cctcacaaag aggaaagatt tctctatcca 960
atttacgggt taataacttt gagtgcgaagt atgcctttt acaaagtgtt gaatctattc

1020 aatagaaagc cgattcttaa aaaaggtata aagttgtcag ttttattaat tgttgtaggc
1080 caggcaatgt cacggatagt ggctttggtg aacaattaca cagctcctat agccgtctac
1140 gagcaatttt cttcactaaa tcaaggtggt gtgaaggcac cggtagtgaa tgtatgtacg
1200 ggacgtgaat ggtatcactt cccaagttct ttctgtctgc cagataatca taggctaaaa
1260 tttgttaaat ctggatttga tggctttctt ccaggtgatt ttccagagag tggttctatt
1320 ttcaaaaaga ttagaacttt acctaaggga atgaataaca agaatatata tgataccggt
1380 aaagagtggc cgatcactag atgtgattat tttattgaca tcgtcgcccc aataaattta
1440 acaaaagacg ttttcaaccc tctacatctg atggataact ggaataagct ggcattgtgt
1500 gcattcatcg acggtgaaaa ttctaagatt ttgggtagag cattttacgt accggagcca
1560 atcaaccgaa tcatgcaa atgttttacca aaacaatgga atcaagtgtg cgggtgttcgt
1620 tacattgatt actgtttgtt tgaaaaacca actgagacta ctaattga
1668

```

<210> SEQ ID NO 51

<211> LENGTH: 555

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 51

```

Met Asn Cys Lys Ala Val Thr Ile Ser Leu Leu Leu Leu Phe Leu
  1           5           10           15
Thr Arg Val Tyr Ile Gln Pro Thr Phe Ser Leu Ile Ser Asp Cys Asp
          20           25           30
Glu Thr Phe Asn Tyr Trp Glu Pro Leu Asn Leu Leu Val Arg Gly Phe

```



```

Thr Lys Asp Val Phe Asn Pro Leu His Leu Met Asp Asn Trp Asn Lys
      485                      490                      495
Leu Ala Cys Ala Ala Phe Ile Asp Gly Glu Asn Ser Lys Ile Leu Gly
      500                      505                      510
Arg Ala Phe Tyr Val Pro Glu Pro Ile Asn Arg Ile Met Gln Ile Val
      515                      520                      525
Leu Pro Lys Gln Trp Asn Gln Val Tyr Gly Val Arg Tyr Ile Asp Tyr
      530                      535                      540
Cys Leu Phe Glu Lys Pro Thr Glu Thr Thr Asn
545                      550                      555

```

<210> SEQ ID NO 52

<211> LENGTH: 600

<212> TYPE: DNA

<213> ORGANISM: *Pichia pastoris*

<400> SEQUENCE: 52

```

tggccttcct gtctgctcga tacttccttt tacagtaacc aacatacatg ttctccaaca 60
tgctcttgta tgtattggcc tattctatct tgagacttga tatcaacctt ctatgggtatt 120
atttcagact gtgatgaagt gttcaactac tgggagccac tcaacttcat gcttagaggg 180
tttggaaaac agacttgga gtattctcca gagtatgcca tccgatcttg gtcctatcta 240
gtgccacttt ggatagcagg ctatccacca ttgttcctgg atatcccttc ttactacttt 300
ttctactttt tcagactact gctgggttatt ttttcattgg ttgcagaagt caagttgtac 360
catagtttga agaaaaatgt cagcagtaag atcagtttct ggtaccttct atttacaacc 420
gttgctccag gaatgtctca tagcacgata gccttattac catcctcttt tgctatgggt 480
tgtcacactt ttgccattag atacgtcatt gattacctac aattaccaac attaatgcgc 540
acaatcagag agactgctgc catctcacca gtcacaaaac aacaactagc caactctctc 600

```

<210> SEQ ID NO 53

<211> LENGTH: 199

<212> TYPE: PRT

<213> ORGANISM: *Pichia pastoris*

<400> SEQUENCE: 53

```

Trp Pro Ser Cys Leu Leu Asp Thr Ser Phe Tyr Ser Asn Gln His Thr
  1           5           10           15
Cys Ser Pro Thr Cys Ser Cys Met Tyr Trp Pro Ile Leu Ser Asp Leu
      20           25           30
Ile Ser Thr Phe Tyr Gly Ile Ile Ser Asp Cys Asp Glu Val Phe Asn
      35           40           45
Tyr Trp Glu Pro Leu Asn Phe Met Leu Arg Gly Phe Gly Lys Gln Thr
      50           55           60
Trp Glu Tyr Ser Pro Glu Tyr Ala Ile Arg Ser Trp Ser Tyr Leu Val
      65           70           75           80
Pro Leu Trp Ile Ala Gly Tyr Pro Pro Leu Phe Leu Asp Ile Pro Ser
      85           90           95
Tyr Tyr Phe Phe Tyr Phe Phe Arg Leu Leu Leu Val Ile Phe Ser Leu
      100          105          110
Val Ala Glu Val Lys Leu Tyr His Ser Leu Lys Lys Asn Val Ser Ser
      115          120          125
Lys Ile Ser Phe Trp Tyr Leu Leu Phe Thr Thr Val Ala Pro Gly Met
      130          135          140
Ser His Ser Thr Ile Ala Leu Leu Pro Ser Ser Phe Ala Met Val Cys
      145          150          155          160
His Thr Phe Ala Ile Arg Tyr Val Ile Asp Tyr Leu Gln Leu Pro Thr
      165          170          175
Leu Met Arg Thr Ile Arg Glu Thr Ala Ala Ile Ser Pro Ala His Lys

```

180 185 190
 Gln Gln Leu Ala Asn Ser Leu
 195

<210> SEQ ID NO 54
 <211> LENGTH: 140
 <212> TYPE: PRT
 <213> ORGANISM: *Pichia pastoris*
 <220> FEATURE:
 <221> NAME/KEY: MOD_RES
 <222> LOCATION: (65)..(71)
 <223> OTHER INFORMATION: Variable amino acid
 <400> SEQUENCE: 54
 Ile Ser Thr Phe Tyr Gly Ile Ile Ser Asp Cys Asp Glu Val Phe Asn
 1 5 10 15
 Tyr Trp Glu Pro Leu Asn Phe Met Leu Arg Gly Phe Gly Lys Gln Thr
 20 25 30
 Trp Glu Tyr Ser Pro Glu Tyr Ala Ile Arg Ser Trp Ser Tyr Leu Val
 35 40 45
 Pro Leu Trp Ile Ala Gly Tyr Pro Pro Leu Phe Leu Asp Ile Pro Ser
 50 55 60
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Leu Leu Val Ile Phe Ser Leu
 65 70 75 80
 Val Ala Glu Val Lys Leu Tyr His Ser Leu Lys Lys Asn Val Ser Ser
 85 90 95
 Lys Ile Ser Phe Trp Tyr Leu Leu Phe Thr Thr Val Ala Pro Gly Met
 100 105 110
 Ser His Ser Thr Ile Ala Leu Leu Pro Ser Ser Phe Ala Met Val Cys
 115 120 125
 His Thr Phe Ala Ile Arg Tyr Val Ile Asp Tyr Leu
 130 135 140

<210> SEQ ID NO 55
 <211> LENGTH: 141
 <212> TYPE: PRT
 <213> ORGANISM: *Saccharomyces cerevisiae*
 <400> SEQUENCE: 55
 Ile Gln Pro Thr Phe Ser Leu Ile Ser Asp Cys Asp Glu Thr Phe Asn
 1 5 10 15
 Tyr Trp Glu Pro Leu Asn Leu Leu Val Arg Gly Phe Gly Lys Gln Thr
 20 25 30
 Trp Glu Tyr Ser Pro Glu Tyr Ser Ile Arg Ser Trp Ala Phe Leu Leu
 35 40 45
 Pro Phe Tyr Cys Ile Leu Tyr Pro Val Asn Lys Phe Thr Asp Leu Glu
 50 55 60
 Ser His Trp Asn Phe Phe Ile Thr Arg Ala Cys Leu Gly Phe Phe Ser
 65 70 75 80
 Phe Ile Met Glu Phe Lys Leu His Arg Glu Ile Ala Gly Ser Leu Ala
 85 90 95
 Leu Gln Ile Ala Asn Ile Trp Ile Ile Phe Gln Leu Phe Asn Pro Gly
 100 105 110
 Trp Phe His Ala Ser Val Glu Leu Leu Pro Ser Ala Val Ala Met Leu
 115 120 125
 Leu Tyr Val Gly Ala Thr Arg His Ser Leu Arg Tyr Leu
 130 135 140

```

<210> SEQ ID NO 56
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Pichia pastoris
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (66)..(72)
<223> OTHER INFORMATION: Variable amino acid
<400> SEQUENCE: 56
  Leu Ile Ser Thr Phe Tyr Gly Ile Ile Ser Asp Cys Asp Glu Val Phe
    1             5             10             15
  Asn Tyr Trp Glu Pro Leu Asn Phe Met Leu Arg Gly Phe Gly Lys Gln
             20             25             30
  Thr Trp Glu Tyr Ser Pro Glu Tyr Ala Ile Arg Ser Trp Ser Tyr Leu
    35             40             45
  Val Pro Leu Trp Ile Ala Gly Tyr Pro Pro Leu Phe Leu Asp Ile Pro
    50             55             60
  Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Leu Leu Val Ile Phe Ser
    65             70             75             80
  Leu Val Ala Glu Val Lys Leu Tyr His Ser Leu Lys Lys Asn Val Ser
             85             90             95
  Ser Lys Ile Ser Phe Trp Tyr Leu Leu Phe Thr Thr Val Ala Pro Gly
             100             105             110
  Met Ser His Ser Thr Ile Ala Leu Leu Pro Ser Ser Phe Ala Met
             115             120             125

```

```

<210> SEQ ID NO 57
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Anopheles gambiae
<400> SEQUENCE: 57
  Leu Gln Ser Ala Leu Tyr Ser Ile Ile Ser Asp Cys Asp Glu Thr Tyr
    1             5             10             15
  Asn Tyr Trp Glu Pro Leu His Tyr Leu Leu Lys Gly Lys Gly Phe Gln
             20             25             30
  Thr Trp Glu Tyr Ser Pro Glu Phe Ala Leu Arg Ser Tyr Ser Tyr Leu
    35             40             45
  Trp Leu His Gly Leu Pro Ala Lys Val Leu Gln Leu Met Thr Asp Asn
    50             55             60
  Gly Val Leu Ile Phe Tyr Phe Val Arg Cys Leu Leu Ala Val Thr Cys
    65             70             75             80
  Ala Leu Leu Glu Tyr Arg Leu Tyr Arg Ile Leu Gly Arg Lys Cys Gly
             85             90             95
  Gly Gly Val Ala Ser Leu Trp Leu Leu Phe Gln Leu Thr Ser Ala Gly
             100             105             110
  Met Phe Ile Ser Ser Ala Ala Leu Leu Pro Ser Ser Phe Ser Met
             115             120             125

```

```

<210> SEQ ID NO 58
<211> LENGTH: 157
<212> TYPE: PRT
<213> ORGANISM: Pichia pastoris
<220> FEATURE:
<221> NAME/KEY: MOD_RES

```

<222> LOCATION: (66)..(72)

<223> OTHER INFORMATION: Variable amino acid

<400> SEQUENCE: 58

```

Leu Ile Ser Thr Phe Tyr Gly Ile Ile Ser Asp Cys Asp Glu Val Phe
 1           5           10           15
Asn Tyr Trp Glu Pro Leu Asn Phe Met Leu Arg Gly Phe Gly Lys Gln
          20           25           30
Thr Trp Glu Tyr Ser Pro Glu Tyr Ala Ile Arg Ser Trp Ser Tyr Leu
          35           40           45
Val Pro Leu Trp Ile Ala Gly Tyr Pro Pro Leu Phe Leu Asp Ile Pro
          50           55           60
Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Leu Leu Val Ile Phe Ser
 65           70           75           80
Leu Val Ala Glu Val Lys Leu Tyr His Ser Leu Lys Lys Asn Val Ser
          85           90           95
Ser Lys Ile Ser Phe Trp Tyr Leu Leu Phe Thr Thr Val Ala Pro Gly
          100          105          110
Met Ser His Ser Thr Ile Ala Leu Leu Pro Ser Ser Phe Ala Met Val
          115          120          125
Cys His Thr Phe Ala Ile Arg Tyr Val Ile Asp Tyr Leu Gln Leu Pro
          130          135          140
Thr Leu Met Arg Thr Ile Arg Glu Thr Ala Ala Ile Ser
145           150           155

```

<210> SEQ ID NO 59

<211> LENGTH: 154

<212> TYPE: PRT

<213> ORGANISM: Schizosaccharomyces pombe

<400> SEQUENCE: 59

```

Leu Thr Ser Ala Ser Phe Arg Val Ile Asp Asp Cys Asp Glu Val Tyr
 1           5           10           15
Asn Tyr Trp Glu Pro Leu His Tyr Leu Leu Tyr Gly Tyr Gly Leu Gln
          20           25           30
Thr Trp Glu Tyr Ser Pro Glu Tyr Ala Ile Arg Ser Trp Phe Tyr Ile
          35           40           45
Ala Leu His Ala Val Pro Gly Phe Leu Ala Arg Gly Leu Gly Leu Ser
          50           55           60
Arg Leu His Val Phe Tyr Phe Ile Arg Gly Val Leu Ala Cys Phe Ser
 65           70           75           80
Ala Phe Cys Glu Thr Asn Leu Ile Leu Ala Val Ala Arg Asn Phe Asn
          85           90           95
Arg Ala Val Ala Leu His Leu Thr Ser Val Leu Phe Val Asn Ser Gly
          100          105          110
Met Trp Ser Ala Ser Thr Ser Phe Leu Pro Ser Ser Phe Ala Met Asn
          115          120          125
Met Val Thr Leu Ala Leu Ser Ala Gln Leu Ser Pro Pro Ser Thr Lys
          130          135          140
Arg Thr Val Lys Val Val Ser Phe Ile Thr
145           150

```

<210> SEQ ID NO 60

<211> LENGTH: 141

<212> TYPE: PRT

<213> ORGANISM: Pichia pastoris

<220> FEATURE:

<221> NAME/KEY: MOD_RES
 <222> LOCATION: (80)..(86)
 <223> OTHER INFORMATION: Variable amino acid
 <400> SEQUENCE: 60
 Ser Pro Thr Cys Ser Cys Met Tyr Trp Pro Ile Leu Ser Asp Leu Ile
 1 5 10 15
 Ser Thr Phe Tyr Gly Ile Ile Ser Asp Cys Asp Glu Val Phe Asn Tyr
 20 25 30
 Trp Glu Pro Leu Asn Phe Met Leu Arg Gly Phe Gly Lys Gln Thr Trp
 35 40 45
 Glu Tyr Ser Pro Glu Tyr Ala Ile Arg Ser Trp Ser Tyr Leu Val Pro
 50 55 60
 Leu Trp Ile Ala Gly Tyr Pro Pro Leu Phe Leu Asp Ile Pro Ser Xaa
 65 70 75 80
 Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Leu Leu Val Ile Phe Ser Leu Val
 85 90 95
 Ala Glu Val Lys Leu Tyr His Ser Leu Lys Lys Asn Val Ser Ser Lys
 100 105 110
 Ile Ser Phe Trp Tyr Leu Leu Phe Thr Thr Val Ala Pro Gly Met Ser
 115 120 125
 His Ser Thr Ile Ala Leu Leu Pro Ser Ser Phe Ala Met
 130 135 140

<210> SEQ ID NO 61
 <211> LENGTH: 143
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <400> SEQUENCE: 61
 Ala Pro Glu Gly Ser Thr Ala Phe Lys Cys Leu Leu Ser Ala Arg Leu
 1 5 10 15
 Cys Ala Ala Leu Leu Ser Asn Ile Ser Asp Cys Asp Glu Thr Phe Asn
 20 25 30
 Tyr Trp Glu Pro Thr His Tyr Leu Ile Tyr Gly Lys Gly Phe Gln Thr
 35 40 45
 Trp Glu Tyr Ser Pro Val Tyr Ala Ile Arg Ser Tyr Ala Tyr Leu Leu
 50 55 60
 Leu His Ala Trp Pro Ala Ala Phe His Ala Arg Ile Leu Gln Thr Asn
 65 70 75 80
 Lys Ile Leu Val Phe Tyr Phe Leu Arg Cys Leu Leu Ala Phe Val Ser
 85 90 95
 Cys Val Cys Glu Leu Tyr Phe Tyr Lys Ala Val Cys Lys Lys Phe Gly
 100 105 110
 Leu His Val Ser Arg Met Met Leu Ala Phe Leu Val Leu Ser Thr Gly
 115 120 125
 Met Phe Cys Ser Ser Ser Ala Phe Leu Pro Ser Ser Phe Cys Met
 130 135 140

<210> SEQ ID NO 62
 <211> LENGTH: 141
 <212> TYPE: PRT
 <213> ORGANISM: Pichia pastoris
 <220> FEATURE:
 <221> NAME/KEY: MOD_RES
 <222> LOCATION: (80)..(86)
 <223> OTHER INFORMATION: Variable amino acid

<400> SEQUENCE: 62

```

Ser Pro Thr Cys Ser Cys Met Tyr Trp Pro Ile Leu Ser Asp Leu Ile
 1           5           10           15
Ser Thr Phe Tyr Gly Ile Ile Ser Asp Cys Asp Glu Val Phe Asn Tyr
          20           25           30
Trp Glu Pro Leu Asn Phe Met Leu Arg Gly Phe Gly Lys Gln Thr Trp
          35           40           45
Glu Tyr Ser Pro Glu Tyr Ala Ile Arg Ser Trp Ser Tyr Leu Val Pro
          50           55           60
Leu Trp Ile Ala Gly Tyr Pro Pro Leu Phe Leu Asp Ile Pro Ser Xaa
          65           70           75           80
Xaa Xaa Xaa Xaa Xaa Xaa Arg Leu Leu Leu Val Ile Phe Ser Leu Val
          85           90           95
Ala Glu Val Lys Leu Tyr His Ser Leu Lys Lys Asn Val Ser Ser Lys
          100          105          110
Ile Ser Phe Trp Tyr Leu Leu Phe Thr Thr Val Ala Pro Gly Met Ser
          115          120          125
His Ser Thr Ile Ala Leu Leu Pro Ser Ser Phe Ala Met
          130          135          140

```

<210> SEQ ID NO 63

<211> LENGTH: 143

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 63

```

Ala Pro Glu Gly Ser Thr Ala Phe Lys Cys Leu Leu Ser Ala Arg Leu
 1           5           10           15
Cys Ala Ala Leu Leu Ser Asn Ile Ser Asp Cys Asp Glu Thr Phe Asn
          20           25           30
Tyr Trp Glu Pro Thr His Tyr Leu Ile Tyr Gly Glu Gly Phe Gln Thr
          35           40           45
Trp Glu Tyr Ser Pro Ala Tyr Ala Ile Arg Ser Tyr Ala Tyr Leu Leu
          50           55           60
Leu His Ala Trp Pro Ala Ala Phe His Ala Arg Ile Leu Gln Thr Asn
          65           70           75           80
Lys Ile Leu Val Phe Tyr Phe Leu Arg Cys Leu Leu Ala Phe Val Ser
          85           90           95
Cys Ile Cys Glu Leu Tyr Phe Tyr Lys Ala Val Cys Lys Lys Phe Gly
          100          105          110
Leu His Val Ser Arg Met Met Leu Ala Phe Leu Val Leu Ser Thr Gly
          115          120          125
Met Phe Cys Ser Ser Ser Ala Phe Leu Pro Ser Ser Phe Cys Met
          130          135          140

```

<210> SEQ ID NO 64

<211> LENGTH: 1656

<212> TYPE: DNA

<213> ORGANISM: Saccharomyces cerevisiae

<400> SEQUENCE: 64

```

atgcggttggt ctgtccttga tacagtgcta ttgaccgtga tttcctttca tctaataccaa 60
gctccattca ccaaggtgga agagagtttt aatattcaag ccattcatga tattttaacc 120
tacagcgtat ttgatatctc ccaatatgac cacttgaaat ttcttgagat agtccctaga 180
acattcgttg gtgctgtgat tattgcaatg ctttcgagac cttatcttta cttgagttct 240
ttgatccaaa cttccaggcc tacgtctata gatgttcaat tggtcgtag ggggattgtt 300
ggcctcacca atgggctttc ttttatctat ttaaagaatt gtttgcaaga tatgtttgat 360

```

```

gaaatcactg aaaagaaaaa ggaagaaaat gaagacaagg atatatacat ttacgatagc 420
gctggtacat ggtttctttt atttttaatt ggcagtttcc acctcatgtt ctacagcact 480
aggactctgc ctaattttgt catgactctg cctctaacca acgtcgcatt ggggtgggtt 540
ttattgggtc gttataatgc agctatatcc ctatctgcgc tcgtggcaat tgtatttaga 600
ctggaagtgt cagctctcag tgctggtatt gctctattta gcgtcatctt caagaagatt 660
tctttattcg atgctatcaa attcgggtatc tttggcttgg gacttggttc cgccatcagt 720
atcaccggtg attcatattt ctggcaagaa tgggtgtctac ctgaggtaga tggtttcttg 780
ttcaacgtgg ttgcgggtta cgcttccaag tgggggtgtg agccagttac tgcttatttc 840
acgcattact tgagaatgat gtttatgcca ccaactgttt tactattgaa ttacttcggc 900
tataaattag cacctgcaaa attaaaaatt gtctcactag catctctttt ccacattatc 960
gtcttatcct ttcaacctca caaagaatgg agattcatca tctacgtgtg tccatctatc

1020 atgttgctag gtgccacagg agcagcacat ctatgggaga atatgaaagt aaaaaagatt
1080 accaatgttt tatgtttggc tatattgccc ttatctataa tgacctcctt tttcatttca
1140 atggcgttct tgtatatatc aagaatgaat tatccaggcg gcgaggcttt aacttctttt
1200 aatgacatga ttgtggaaaa aaatattaca aacgctacag ttcatatcag catacctcct
1260 tgcattgacag gtgtcacttt atttggtgaa ttgaactacg gtgtgtacgg catcaattac
1320 gataagactg aaaatacgac tttactgcag gaaatgtggc cctcctttga tttcttgatc
1380 acccacgagc caaccgcctc tcaattgcca ttcgagaata agactaccaa ccattgggag
1440 ctagttaaca caacaaagat gtttactgga tttgacccaa cctacattaa gaactttggt
1500 ttccaagaga gagtgaatgt tttgtctcta ctcaaacaga tcatttttga caagaccctt
1560 accgtttttt tgaaagaatt gacggccaat tcgattgtta aaagcgatgt cttcttcacc
1620 tataagagaa tcaaacaaga tgaaaaaact gattga
1656

```

<210> SEQ ID NO 65

<211> LENGTH: 551

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 65

```

Met Arg Trp Ser Val Leu Asp Thr Val Leu Leu Thr Val Ile Ser Phe
 1           5           10           15
His Leu Ile Gln Ala Pro Phe Thr Lys Val Glu Glu Ser Phe Asn Ile
          20           25           30
Gln Ala Ile His Asp Ile Leu Thr Tyr Ser Val Phe Asp Ile Ser Gln
          35           40           45
Tyr Asp His Leu Lys Phe Pro Gly Val Val Pro Arg Thr Phe Val Gly
          50           55           60
Ala Val Ile Ile Ala Met Leu Ser Arg Pro Tyr Leu Tyr Leu Ser Ser
          65           70           75           80
Leu Ile Gln Thr Ser Arg Pro Thr Ser Ile Asp Val Gln Leu Val Val
          85           90           95
Arg Gly Ile Val Gly Leu Thr Asn Gly Leu Ser Phe Ile Tyr Leu Lys
          100          105          110
Asn Cys Leu Gln Asp Met Phe Asp Glu Ile Thr Glu Lys Lys Lys Glu

```

		115					120					125					
Glu	Asn	Glu	Asp	Lys	Asp	Ile	Tyr	Ile	Tyr	Asp	Ser	Ala	Gly	Thr	Trp		
	130					135					140						
Phe	Leu	Leu	Phe	Leu	Ile	Gly	Ser	Phe	His	Leu	Met	Phe	Tyr	Ser	Thr		
145					150					155					160		
Arg	Thr	Leu	Pro	Asn	Phe	Val	Met	Thr	Leu	Pro	Leu	Thr	Asn	Val	Ala		
				165					170					175			
Leu	Gly	Trp	Val	Leu	Leu	Gly	Arg	Tyr	Asn	Ala	Ala	Ile	Phe	Leu	Ser		
			180					185					190				
Ala	Leu	Val	Ala	Ile	Val	Phe	Arg	Leu	Glu	Val	Ser	Ala	Leu	Ser	Ala		
	195					200						205					
Gly	Ile	Ala	Leu	Phe	Ser	Val	Ile	Phe	Lys	Lys	Ile	Ser	Leu	Phe	Asp		
	210					215					220						
Ala	Ile	Lys	Phe	Gly	Ile	Phe	Gly	Leu	Gly	Leu	Gly	Ser	Ala	Ile	Ser		
225					230					235					240		
Ile	Thr	Val	Asp	Ser	Tyr	Phe	Trp	Gln	Glu	Trp	Cys	Leu	Pro	Glu	Val		
			245						250					255			
Asp	Gly	Phe	Leu	Phe	Asn	Val	Val	Ala	Gly	Tyr	Ala	Ser	Lys	Trp	Gly		
			260					265					270				
Val	Glu	Pro	Val	Thr	Ala	Tyr	Phe	Thr	His	Tyr	Leu	Arg	Met	Met	Phe		
	275					280						285					
Met	Pro	Pro	Thr	Val	Leu	Leu	Leu	Asn	Tyr	Phe	Gly	Tyr	Lys	Leu	Ala		
	290				295						300						
Pro	Ala	Lys	Leu	Lys	Ile	Val	Ser	Leu	Ala	Ser	Leu	Phe	His	Ile	Ile		
305					310					315					320		
Val	Leu	Ser	Phe	Gln	Pro	His	Lys	Glu	Trp	Arg	Phe	Ile	Ile	Tyr	Ala		
				325					330					335			
Val	Pro	Ser	Ile	Met	Leu	Leu	Gly	Ala	Thr	Gly	Ala	Ala	His	Leu	Trp		
			340					345					350				
Glu	Asn	Met	Lys	Val	Lys	Lys	Ile	Thr	Asn	Val	Leu	Cys	Leu	Ala	Ile		
	355					360						365					
Leu	Pro	Leu	Ser	Ile	Met	Thr	Ser	Phe	Phe	Ile	Ser	Met	Ala	Phe	Leu		
	370				375						380						
Tyr	Ile	Ser	Arg	Met	Asn	Tyr	Pro	Gly	Gly	Glu	Ala	Leu	Thr	Ser	Phe		
385					390					395					400		
Asn	Asp	Met	Ile	Val	Glu	Lys	Asn	Ile	Thr	Asn	Ala	Thr	Val	His	Ile		
				405					410					415			
Ser	Ile	Pro	Pro	Cys	Met	Thr	Gly	Val	Thr	Leu	Phe	Gly	Glu	Leu	Asn		
			420					425					430				
Tyr	Gly	Val	Tyr	Gly	Ile	Asn	Tyr	Asp	Lys	Thr	Glu	Asn	Thr	Thr	Leu		
	435					440						445					
Leu	Gln	Glu	Met	Trp	Pro	Ser	Phe	Asp	Phe	Leu	Ile	Thr	His	Glu	Pro		
	450					455					460						
Thr	Ala	Ser	Gln	Leu	Pro	Phe	Glu	Asn	Lys	Thr	Thr	Asn	His	Trp	Glu		
465					470					475					480		
Leu	Val	Asn	Thr	Thr	Lys	Met	Phe	Thr	Gly	Phe	Asp	Pro	Thr	Tyr	Ile		
				485					490					495			
Lys	Asn	Phe	Val	Phe	Gln	Glu	Arg	Val	Asn	Val	Leu	Ser	Leu	Leu	Lys		
			500					505					510				
Gln	Ile	Ile	Phe	Asp	Lys	Thr	Pro	Thr	Val	Phe	Leu	Lys	Glu	Leu	Thr		
	515					520						525					
Ala	Asn	Ser	Ile	Val	Lys	Ser	Asp	Val	Phe	Phe	Thr	Tyr	Lys	Arg	Ile		
	530					535					540						
Lys	Gln	Asp	Glu	Lys	Thr	Asp											
545					550												

<210> SEQ ID NO 66

<211> LENGTH: 840

<212> TYPE: DNA

<213> ORGANISM: *Pichia pastoris*

<400> SEQUENCE: 66

```

tcggtcgaga atgataactg aagaactcaa aatctctcac actttcatcg ttactgtact 60
ggcaatcatt gcatttcagc ctcataaaga atggagattt atagtttaca ttgttccacc 120
acttgatcatc accatatcta cagtacttgc acaactaccc aggagattca caatcgtcaa 180
agttgctgtt tttctcctaa gtttcggctc tttgctcata tccctgtcgt ttcttttcat 240
ctcatcgtat aactaccctg ggggtgaagc tttacagcat ttgaacgaga aactccttct 300
actggaccaa agttccctac ctgttgatat taaggttcat atggatgtcc ctgcatgcat 360
gactggggtg actttatttg gttacttgga taactcaaaa ttgaacaatt taagaattgt 420
ctatgataaa acagaagacg agtcgctgga cacaatctgg gattctttca attatgtcat 480
ctccgaaatt gacttggatt cttcgactgc tcccaaattg gagggggatt ggctgaagat 540
tgatgttgtc caaggctaca acggcatcaa taaacaatct atcaaaaata caattttcaa 600
ttatggaata cttaaacgga tgataagaga cgcaaccaa cttgatgttg gatttattcg 660
tacggctctt cgatccttca taaaatttga tgataaatta ttcatttatg agaggagcag 720
tcaaacctga aaatatatac ctcatctgtt caatttggtg taaagagtgt ggcggataga 780
cttcttgtaa atcaggaaag ctacaattcc aattgctgca aaaaatacca atgcccataa 840

```

<210> SEQ ID NO 67

<211> LENGTH: 239

<212> TYPE: PRT

<213> ORGANISM: *Pichia pastoris*

<400> SEQUENCE: 67

```

Arg Met Ile Thr Glu Glu Leu Lys Ile Ser His Thr Phe Ile Val Thr
 1           5           10           15
Val Leu Ala Ile Ile Ala Phe Gln Pro His Lys Glu Trp Arg Phe Ile
          20           25           30
Val Tyr Ile Val Pro Pro Leu Val Ile Thr Ile Ser Thr Val Leu Ala
          35           40           45
Gln Leu Pro Arg Arg Phe Thr Ile Val Lys Val Ala Val Phe Leu Leu
          50           55           60
Ser Phe Gly Ser Leu Leu Ile Ser Leu Ser Phe Leu Phe Ile Ser Ser
          65           70           75           80
Tyr Asn Tyr Pro Gly Gly Glu Ala Leu Gln His Leu Asn Glu Lys Leu
          85           90           95
Leu Leu Leu Asp Gln Ser Ser Leu Pro Val Asp Ile Lys Val His Met
          100          105          110
Asp Val Pro Ala Cys Met Thr Gly Val Thr Leu Phe Gly Tyr Leu Asp
          115          120          125
Asn Ser Lys Leu Asn Asn Leu Arg Ile Val Tyr Asp Lys Thr Glu Asp
          130          135          140
Glu Ser Leu Asp Thr Ile Trp Asp Ser Phe Asn Tyr Val Ile Ser Glu
          145          150          155          160
Ile Asp Leu Asp Ser Ser Thr Ala Pro Lys Trp Glu Gly Asp Trp Leu
          165          170          175
Lys Ile Asp Val Val Gln Gly Tyr Asn Gly Ile Asn Lys Gln Ser Ile
          180          185          190
Lys Asn Thr Ile Phe Asn Tyr Gly Ile Leu Lys Arg Met Ile Arg Asp
          195          200          205
Ala Thr Lys Leu Asp Val Gly Phe Ile Arg Thr Val Phe Arg Ser Phe
          210          215          220
Ile Lys Phe Asp Asp Lys Leu Phe Ile Tyr Glu Arg Ser Ser Gln

```

```

225                               230                               235

<210> SEQ ID NO 68
<211> LENGTH: 239
<212> TYPE: PRT
<213> ORGANISM: Pichia pastoris
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (62)..(80)
<223> OTHER INFORMATION: Variable amino acid
<400> SEQUENCE: 68
  Arg Met Ile Thr Glu Glu Leu Lys Ile Ser His Thr Phe Ile Val Thr
    1                               5                               10                               15
  Val Leu Ala Ile Ile Ala Phe Gln Pro His Lys Glu Trp Arg Phe Ile
                20                               25                               30
  Val Tyr Ile Val Pro Pro Leu Val Ile Thr Ile Ser Thr Val Leu Ala
    35                               40                               45
  Gln Leu Pro Arg Arg Phe Thr Ile Val Lys Val Ala Val Xaa Xaa Xaa
    50                               55                               60
  Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    65                               70                               75                               80
  Tyr Asn Tyr Pro Gly Gly Glu Ala Leu Gln His Leu Asn Glu Lys Leu
                85                               90                               95
  Leu Leu Leu Asp Gln Ser Ser Leu Pro Val Asp Ile Lys Val His Met
    100                               105                               110
  Asp Val Pro Ala Cys Met Thr Gly Val Thr Leu Phe Gly Tyr Leu Asp
    115                               120                               125
  Asn Ser Lys Leu Asn Asn Leu Arg Ile Val Tyr Asp Lys Thr Glu Asp
    130                               135                               140
  Glu Ser Leu Asp Thr Ile Trp Asp Ser Phe Asn Tyr Val Ile Ser Glu
    145                               150                               155                               160
  Ile Asp Leu Asp Ser Ser Thr Ala Pro Lys Trp Glu Gly Asp Trp Leu
                165                               170                               175
  Lys Ile Asp Val Val Gln Gly Tyr Asn Gly Ile Asn Lys Gln Ser Ile
    180                               185                               190
  Lys Asn Thr Ile Phe Asn Tyr Gly Ile Leu Lys Arg Met Ile Arg Asp
    195                               200                               205
  Ala Thr Lys Leu Asp Val Gly Phe Ile Arg Thr Val Phe Arg Ser Phe
    210                               215                               220
  Ile Lys Phe Asp Asp Lys Leu Phe Ile Tyr Glu Arg Ser Ser Gln
    225                               230                               235

```

```

<210> SEQ ID NO 69
<211> LENGTH: 245
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces cerevisiae
<400> SEQUENCE: 69
  Lys Leu Ala Pro Ala Lys Leu Lys Ile Val Ser Leu Ala Ser Leu Phe
    1                               5                               10                               15
  His Ile Ile Val Leu Ser Phe Gln Pro His Lys Glu Trp Arg Phe Ile
                20                               25                               30
  Ile Tyr Ala Val Pro Ser Ile Met Leu Leu Gly Ala Thr Gly Ala Ala
    35                               40                               45
  His Leu Trp Glu Asn Met Lys Val Lys Lys Ile Thr Asn Val Leu Cys
    50                               55                               60

```

```

Leu Ala Ile Leu Pro Leu Ser Ile Met Thr Ser Phe Phe Ile Ser Met
 65          70          75          80
Ala Phe Leu Tyr Ile Ser Arg Met Asn Tyr Pro Gly Gly Glu Ala Leu
          85          90          95
Thr Ser Phe Asn Asp Met Ile Val Glu Lys Asn Ile Thr Asn Ala Thr
          100          105          110
Val His Ile Ser Ile Pro Pro Cys Met Thr Gly Val Thr Leu Phe Gly
          115          120          125
Glu Leu Asn Tyr Gly Val Tyr Gly Ile Asn Tyr Asp Lys Thr Glu Asn
          130          135          140
Thr Thr Leu Leu Gln Glu Met Trp Pro Ser Phe Asp Phe Leu Ile Thr
          145          150          155          160
His Glu Pro Thr Ala Ser Gln Leu Pro Phe Glu Asn Lys Thr Thr Asn
          165          170          175
His Trp Glu Leu Val Asn Thr Thr Lys Met Phe Thr Gly Phe Asp Pro
          180          185          190
Thr Tyr Ile Lys Asn Phe Val Phe Gln Glu Arg Val Asn Val Leu Ser
          195          200          205
Leu Leu Lys Gln Ile Ile Phe Asp Lys Thr Pro Thr Val Phe Leu Lys
          210          215          220
Glu Leu Thr Ala Asn Ser Ile Val Lys Ser Asp Val Phe Phe Thr Tyr
          225          230          235          240
Lys Arg Ile Lys Gln
          245

```

<210> SEQ ID NO 70

<211> LENGTH: 141

<212> TYPE: PRT

<213> ORGANISM: *Pichia pastoris*

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: (43)..(61)

<223> OTHER INFORMATION: Variable amino acid

<400> SEQUENCE: 70

```

Ile Ile Ala Phe Gln Pro His Lys Glu Trp Arg Phe Ile Val Tyr Ile
 1          5          10          15
Val Pro Pro Leu Val Ile Thr Ile Ser Thr Val Leu Ala Gln Leu Pro
          20          25          30
Arg Arg Phe Thr Ile Val Lys Val Ala Val Xaa Xaa Xaa Xaa Xaa Xaa
          35          40          45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Asn Tyr
          50          55          60
Pro Gly Gly Glu Ala Leu Gln His Leu Asn Glu Lys Leu Leu Leu Leu
          65          70          75          80
Asp Gln Ser Ser Leu Pro Val Asp Ile Lys Val His Met Asp Val Pro
          85          90          95
Ala Cys Met Thr Gly Val Thr Leu Phe Gly Tyr Leu Asp Asn Ser Lys
          100          105          110
Leu Asn Asn Leu Arg Ile Val Tyr Asp Lys Thr Glu Asp Glu Ser Leu
          115          120          125
Asp Thr Ile Trp Asp Ser Phe Asn Tyr Val Ile Ser Glu
          130          135          140

```

<210> SEQ ID NO 71

<211> LENGTH: 137

```

<212> TYPE: PRT
<213> ORGANISM: Schizosaccharomyces pombe
<400> SEQUENCE: 71
Val Tyr Ser Phe Leu Gly His Lys Glu Trp Arg Phe Ile Ile Tyr Ser
 1           5           10           15
Ile Pro Trp Phe Asn Ala Ala Ser Ala Ile Gly Ala Ser Leu Cys Phe
           20           25           30
Asn Ala Ser Lys Phe Gly Lys Lys Ile Phe Glu Ile Leu Arg Leu Met
           35           40           45
Phe Phe Ser Gly Ile Ile Phe Gly Phe Ile Gly Ser Ser Phe Leu Leu
           50           55           60
Tyr Val Phe Gln Tyr Ala Tyr Pro Gly Gly Leu Ala Leu Thr Arg Leu
           65           70           75           80
Tyr Glu Ile Glu Asn His Pro Gln Val Ser Val His Met Asp Val Tyr
           85           90           95
Pro Cys Met Thr Gly Ile Thr Arg Phe Ser Gln Leu Pro Ser Trp Tyr
           100          105          110
Tyr Asp Lys Thr Glu Asp Pro Lys Met Leu Ser Asn Ser Leu Phe Ile
           115          120          125
Ser Gln Phe Asp Tyr Leu Ile Thr Glu
           130          135

```

```

<210> SEQ ID NO 72
<211> LENGTH: 143
<212> TYPE: PRT
<213> ORGANISM: Pichia pastoris
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (45)..(63)
<223> OTHER INFORMATION: Variable amino acid
<400> SEQUENCE: 72
Leu Ala Ile Ile Ala Phe Gln Pro His Lys Glu Trp Arg Phe Ile Val
 1           5           10           15
Tyr Ile Val Pro Pro Leu Val Ile Thr Ile Ser Thr Val Leu Ala Gln
           20           25           30
Leu Pro Arg Arg Phe Thr Ile Val Lys Val Ala Val Xaa Xaa Xaa Xaa
           35           40           45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr
           50           55           60
Asn Tyr Pro Gly Gly Glu Ala Leu Gln His Leu Asn Glu Lys Leu Leu
           65           70           75           80
Leu Leu Asp Gln Ser Ser Leu Pro Val Asp Ile Lys Val His Met Asp
           85           90           95
Val Pro Ala Cys Met Thr Gly Val Thr Leu Phe Gly Tyr Leu Asp Asn
           100          105          110
Ser Lys Leu Asn Asn Leu Arg Ile Val Tyr Asp Lys Thr Glu Asp Glu
           115          120          125
Ser Leu Asp Thr Ile Trp Asp Ser Phe Asn Tyr Val Ile Ser Glu
           130          135          140

```

```

<210> SEQ ID NO 73
<211> LENGTH: 137
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 73

```



```

Met Ala Leu Tyr Ser Leu Leu Pro His Lys Glu Leu Arg Phe Ile Ile
 1           5           10           15
Tyr Ala Phe Pro Met Leu Asn Ile Thr Ala Ala Arg Gly Cys Ser Tyr
          20           25           30
Leu Leu Asn Asn Tyr Lys Lys Ser Trp Leu Tyr Lys Ala Gly Ser Leu
          35           40           45
Leu Val Ile Gly His Leu Val Val Asn Ala Ala Tyr Ser Ala Thr Ala
          50           55           60
Leu Tyr Val Ser His Phe Asn Tyr Pro Gly Gly Val Ala Met Gln Arg
          65           70           75           80
Leu His Gln Leu Val Pro Pro Gln Thr Asp Val Leu Leu His Ile Asp
          85           90           95
Val Ala Ala Ala Gln Thr Gly Val Ser Arg Phe Leu Gln Val Asn Ser
          100          105          110
Ala Trp Arg Tyr Asp Lys Arg Glu Asp Val Gln Pro Gly Thr Gly Met
          115          120          125
Leu Ala Tyr Thr His Ile Leu Met Glu
          130          135

```

<210> SEQ ID NO 74

<211> LENGTH: 1635

<212> TYPE: DNA

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 74

```

atggccattg gcaaaagggtt actggtgaac aaaccagcag aagaatcatt ttatgcttct 60
ccaatgtatg attttttgta tccgttttagg ccagtgggga accaatggct gccagaatat 120
attatctttg tatgtgctgt aatactgagg tgcacaattg gacttggtcc atattctggg 180
aaaggcagtc caccgctgta cggcgatttt gaggtcaga gacattggat ggaaattacg 240
caacattttac cgcttttctaa gtggtactgg tatgatttgc aatactgggg attggactat 300
ccaccattaa cagcatttca ttcgtacctt ctgggcctaa ttggatcttt tttcaatcca 360
tcttggtttg cactagaaaa gtcacgtggc tttgaatccc ccgataatgg cctgaaaaca 420
tatatgcgtt ctactgtcat cattagcgac atattgtttt actttcctgc agtaatatat 480
tttactaagt ggcttggtag atatcgaaac cagtcgccc a taggacaatc tattgcggca 540
tcagcgattt tgttccaacc ttcattaatg ctcatggacc atgggcactt tcaatataat 600
tcagtcatgc ttggccttac tgcttatgcc ataaataact tattagatga gtattatgct 660
atggcgggccg tttgttttgt cctatccatt tgttttaaac aaatggcatt gtattatgca 720
ccgatttttt ttgcttatct attaatgcga tcattgctgt tccccaaatt taacatagct 780
agattgacgg ttattgcgtt tgcaacactc gcaacttttg ctataatatt tgcgccatta 840
tattttcttg gaggaggatt aaagaatatt caccaatgta ttcacaggat attccctttt 900
gccaggggca tcttcgaaga caaggttgct aacttctggt gcgttacgaa cgtgtttgta 960
aaatacaagg aaagattcac tatacaacaa ctccagctat attcattgat tgccaccgtg

1020 attgggtttct taccagccat gataatgaca ttacttcac ccaaaaagca ttttctccca
1080 tacgtgttaa tcgcatgttc gatgtccttt tttcttttta gctttcaagt acatgagaaa
1140 actatcctca tcccactttt gcctattaca ctactctact cctctactga ttggaatggt
1200 ctatctcttg taagttggat aaacaatgtg gctttgttta cgctatggcc tttgttgaaa
1260 aaggacggtc ttcatttaca gtatgccgta tctttcttac taagcaattg gctgattgga
1320 aatttcagtt ttattacacc aaggttcttg ccaaaatctt taactcctgg cccttctatc
1380

```

```

1440   agcagcatca atagcgacta tagaagaaga agcttactgc catataatgt ggtttggaaa
1500   agttttatca taggaacgta tattgctatg ggcttttatc atttcttaga tcaatttgta
1560   gcacctccat cgaaatatcc agacttgtgg gtgttggtga actgtgctgt tgggttcatt
1620   tgcttttagca tattttggct atggtcttat tacaagatat tcacttccgg tagcaaatcc
1635   atgaaggact tgtag

```

```

<210> SEQ ID NO 75
<211> LENGTH: 544
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces cerevisiae
<400> SEQUENCE: 75

```

```

Met Ala Ile Gly Lys Arg Leu Leu Val Asn Lys Pro Ala Glu Glu Ser
  1           5           10           15
Phe Tyr Ala Ser Pro Met Tyr Asp Phe Leu Tyr Pro Phe Arg Pro Val
          20           25           30
Gly Asn Gln Trp Leu Pro Glu Tyr Ile Ile Phe Val Cys Ala Val Ile
          35           40           45
Leu Arg Cys Thr Ile Gly Leu Gly Pro Tyr Ser Gly Lys Gly Ser Pro
          50           55           60
Pro Leu Tyr Gly Asp Phe Glu Ala Gln Arg His Trp Met Glu Ile Thr
          65           70           75           80
Gln His Leu Pro Leu Ser Lys Trp Tyr Trp Tyr Asp Leu Gln Tyr Trp
          85           90           95
Gly Leu Asp Tyr Pro Pro Leu Thr Ala Phe His Ser Tyr Leu Leu Gly
          100          105          110
Leu Ile Gly Ser Phe Phe Asn Pro Ser Trp Phe Ala Leu Glu Lys Ser
          115          120          125
Arg Gly Phe Glu Ser Pro Asp Asn Gly Leu Lys Thr Tyr Met Arg Ser
          130          135          140
Thr Val Ile Ile Ser Asp Ile Leu Phe Tyr Phe Pro Ala Val Ile Tyr
          145          150          155          160
Phe Thr Lys Trp Leu Gly Arg Tyr Arg Asn Gln Ser Pro Ile Gly Gln
          165          170          175
Ser Ile Ala Ala Ser Ala Ile Leu Phe Gln Pro Ser Leu Met Leu Ile
          180          185          190
Asp His Gly His Phe Gln Tyr Asn Ser Val Met Leu Gly Leu Thr Ala
          195          200          205
Tyr Ala Ile Asn Asn Leu Leu Asp Glu Tyr Tyr Ala Met Ala Ala Val
          210          215          220
Cys Phe Val Leu Ser Ile Cys Phe Lys Gln Met Ala Leu Tyr Tyr Ala
          225          230          235          240
Pro Ile Phe Phe Ala Tyr Leu Leu Ser Arg Ser Leu Leu Phe Pro Lys
          245          250          255
Phe Asn Ile Ala Arg Leu Thr Val Ile Ala Phe Ala Thr Leu Ala Thr
          260          265          270
Phe Ala Ile Ile Phe Ala Pro Leu Tyr Phe Leu Gly Gly Gly Leu Lys
          275          280          285
Asn Ile His Gln Cys Ile His Arg Ile Phe Pro Phe Ala Arg Gly Ile
          290          295          300
Phe Glu Asp Lys Val Ala Asn Phe Trp Cys Val Thr Asn Val Phe Val

```

305					310					315				320	
Lys	Tyr	Lys	Glu	Arg	Phe	Thr	Ile	Gln	Gln	Leu	Gln	Leu	Tyr	Ser	Leu
				325					330					335	
Ile	Ala	Thr	Val	Ile	Gly	Phe	Leu	Pro	Ala	Met	Ile	Met	Thr	Leu	Leu
			340					345					350		
His	Pro	Lys	Lys	His	Leu	Leu	Pro	Tyr	Val	Leu	Ile	Ala	Cys	Ser	Met
		355					360					365			
Ser	Phe	Phe	Leu	Phe	Ser	Phe	Gln	Val	His	Glu	Lys	Thr	Ile	Leu	Ile
	370					375					380				
Pro	Leu	Leu	Pro	Ile	Thr	Leu	Leu	Tyr	Ser	Ser	Thr	Asp	Trp	Asn	Val
385				390						395					400
Leu	Ser	Leu	Val	Ser	Trp	Ile	Asn	Asn	Val	Ala	Leu	Phe	Thr	Leu	Trp
			405						410					415	
Pro	Leu	Leu	Lys	Lys	Asp	Gly	Leu	His	Leu	Gln	Tyr	Ala	Val	Ser	Phe
			420					425					430		
Leu	Leu	Ser	Asn	Trp	Leu	Ile	Gly	Asn	Phe	Ser	Phe	Ile	Thr	Pro	Arg
		435					440					445			
Phe	Leu	Pro	Lys	Ser	Leu	Thr	Pro	Gly	Pro	Ser	Ile	Ser	Ser	Ile	Asn
	450					455					460				
Ser	Asp	Tyr	Arg	Arg	Arg	Ser	Leu	Leu	Pro	Tyr	Asn	Val	Val	Trp	Lys
465				470						475					480
Ser	Phe	Ile	Ile	Gly	Thr	Tyr	Ile	Ala	Met	Gly	Phe	Tyr	His	Phe	Leu
			485						490					495	
Asp	Gln	Phe	Val	Ala	Pro	Pro	Ser	Lys	Tyr	Pro	Asp	Leu	Trp	Val	Leu
			500					505					510		
Leu	Asn	Cys	Ala	Val	Gly	Phe	Ile	Cys	Phe	Ser	Ile	Phe	Trp	Leu	Trp
		515					520					525			
Ser	Tyr	Tyr	Lys	Ile	Phe	Thr	Ser	Gly	Ser	Lys	Ser	Met	Lys	Asp	Leu
	530					535					540				

<210> SEQ ID NO 76

<211> LENGTH: 1644

<212> TYPE: DNA

<213> ORGANISM: Pichia pastoris

<400> SEQUENCE: 76

```

atgccacata aaagaacgcc ctctagcagt ctgctgtatg caagaattcc agggatctct 60
tttgaaaact ctccggtggt tgattttttg tctccttttg gaccgctcc taatcaatgg 120
gtagcacgat acatcatcat catcttttgc atttcatca gattggcagt tgggctgggc 180
tcctattccg gcttcaacac cctccaatg tatggggatt ttgaagctca gaggcattgg 240
atggaaatta ctcagcattt atccatagaa aaatggtact tctacgactt gcaatattgg 300
gggcttgact atcctccctt gacagccttt cattcatact tctttggcaa attaggcagc 360
ttcatcaatc cagcatgggt tgcttttagac gtctccagag gggttgaatc agtggatcta 420
aaatcgta ca tgaggcgac cgcaattctc agtgagctgt tatgttttat tccagctgtc 480
at ttggtatt gtcgttggt gggacttaac tacttcaatc aaaacgccat tgagcaaact 540
ataatagcgt ctgctattct tttcaatcca tctttaatta tcatagatca tggccacttc 600
cagtacaact cagttatgct aggttttgct ttattatcca tattaatct gttgtacgat 660
aat tttgcat tagcggctat ttttttcgtt ctttcaataa gctttaagca aatggctctc 720
tattatagcc ccatcatggt tttttacatg ctgagtgtga gttgttggcc tttgaaaaac 780
ttcaacttgt tgagattggc tactatcagt attgcagtac tcttgacttt tgcaactcta 840
ttactgcctt ttgtattagt agatgggatg tcacaaattg gccaaatatt attcagagtt 900
ttcccgtttt caagaggctt gtttgaggat aagggtggcca acttttggtg tacaacgaat 960
atactggtaa agtacaaaca gttattcact gacaaaaccc ttactaggat atcgctagta

1020 gcaactttga ttgcaattag tccgtcttgc ttcatcattt ttactacccc aaagaaggtt
1080

```

```

1140 ttactaccgt gggcttttgc tgcttgcctc tgggcgttct atcttttctc tttccaagtc
1200 cactagaaaat cagtttttagt tccattgatg cctaccactc tattactggg agaaaaagac
1260 ttggacatca tctcaatggg ctgctggatt tctaataattg ccttcttcag catgtggcct
1320 ctattaaaaa gagacgggct ggctttggaa tattttgtct tgggaatatt gagtaattgg
1380 ctgattggaa acctcaattg gattagtaaa tggcttgtcc ccagtttctt gattccaggg
1440 cctactctct ccaaaaaagt tcctaaaaga gatactaaaa cagttgttca tactcactgg
1500 ttttgggggt cagtaacatt cgtttcatac ctcggagcta cagttatcca gtctgtagat
1560 tggctgtacc ttccacctgc caagtatcca gatttgtggg ttattttgaa cactacattg
1620 tcgtttgctt gtttcgggtt gttttggcta tggattaact acaatctgta cattttgcgt
1644 gattttaagc ttaaagatgc ttag

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<210> SEQ ID NO 77

<211> LENGTH: 547

<212> TYPE: PRT

<213> ORGANISM: *Pichia pastoris*

<400> SEQUENCE: 77

```

Met Pro His Lys Arg Thr Pro Ser Ser Ser Leu Leu Tyr Ala Arg Ile
 1          5          10          15
Pro Gly Ile Ser Phe Glu Asn Ser Pro Val Phe Asp Phe Leu Ser Pro
          20          25          30
Phe Gly Pro Ala Pro Asn Gln Trp Val Ala Arg Tyr Ile Ile Ile Ile
          35          40          45
Phe Ala Ile Leu Ile Arg Leu Ala Val Gly Leu Gly Ser Tyr Ser Gly
          50          55          60
Phe Asn Thr Pro Pro Met Tyr Gly Asp Phe Glu Ala Gln Arg His Trp
          65          70          75          80
Met Glu Ile Thr Gln His Leu Ser Ile Glu Lys Trp Tyr Phe Tyr Asp
          85          90          95
Leu Gln Tyr Trp Gly Leu Asp Tyr Pro Pro Leu Thr Ala Phe His Ser
          100          105          110
Tyr Phe Phe Gly Lys Leu Gly Ser Phe Ile Asn Pro Ala Trp Phe Ala
          115          120          125
Leu Asp Val Ser Arg Gly Phe Glu Ser Val Asp Leu Lys Ser Tyr Met
          130          135          140
Arg Ala Thr Ala Ile Leu Ser Glu Leu Leu Cys Phe Ile Pro Ala Val
          145          150          155          160
Ile Trp Tyr Cys Arg Trp Met Gly Leu Asn Tyr Phe Asn Gln Asn Ala
          165          170          175
Ile Glu Gln Thr Ile Ile Ala Ser Ala Ile Leu Phe Asn Pro Ser Leu
          180          185          190
Ile Ile Ile Asp His Gly His Phe Gln Tyr Asn Ser Val Met Leu Gly
          195          200          205
Phe Ala Leu Leu Ser Ile Leu Asn Leu Leu Tyr Asp Asn Phe Ala Leu
          210          215          220
Ala Ala Ile Phe Phe Val Leu Ser Ile Ser Phe Lys Gln Met Ala Leu

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```

225          230          235          240
Tyr Tyr Ser Pro Ile Met Phe Phe Tyr Met Leu Ser Val Ser Cys Trp
          245          250          255
Pro Leu Lys Asn Phe Asn Leu Leu Arg Leu Ala Thr Ile Ser Ile Ala
          260          265          270
Val Leu Leu Thr Phe Ala Thr Leu Leu Leu Pro Phe Val Leu Val Asp
          275          280          285
Gly Met Ser Gln Ile Gly Gln Ile Leu Phe Arg Val Phe Pro Phe Ser
          290          295          300
Arg Gly Leu Phe Glu Asp Lys Val Ala Asn Phe Trp Cys Thr Thr Asn
305          310          315          320
Ile Leu Val Lys Tyr Lys Gln Leu Phe Thr Asp Lys Thr Leu Thr Arg
          325          330          335
Ile Ser Leu Val Ala Thr Leu Ile Ala Ile Ser Pro Ser Cys Phe Ile
          340          345          350
Ile Phe Thr His Pro Lys Lys Val Leu Leu Pro Trp Ala Phe Ala Ala
          355          360          365
Cys Ser Trp Ala Phe Tyr Leu Phe Ser Phe Gln Val His Glu Lys Ser
          370          375          380
Val Leu Val Pro Leu Met Pro Thr Thr Leu Leu Leu Val Glu Lys Asp
385          390          395          400
Leu Asp Ile Ile Ser Met Val Cys Trp Ile Ser Asn Ile Ala Phe Phe
          405          410          415
Ser Met Trp Pro Leu Leu Lys Arg Asp Gly Leu Ala Leu Glu Tyr Phe
          420          425          430
Val Leu Gly Ile Leu Ser Asn Trp Leu Ile Gly Asn Leu Asn Trp Ile
          435          440          445
Ser Lys Trp Leu Val Pro Ser Phe Leu Ile Pro Gly Pro Thr Leu Ser
          450          455          460
Lys Lys Val Pro Lys Arg Asp Thr Lys Thr Val Val His Thr His Trp
465          470          475          480
Phe Trp Gly Ser Val Thr Phe Val Ser Tyr Leu Gly Ala Thr Val Ile
          485          490          495
Gln Phe Val Asp Trp Leu Tyr Leu Pro Pro Ala Lys Tyr Pro Asp Leu
          500          505          510
Trp Val Ile Leu Asn Thr Thr Leu Ser Phe Ala Cys Phe Gly Leu Phe
          515          520          525
Trp Leu Trp Ile Asn Tyr Asn Leu Tyr Ile Leu Arg Asp Phe Lys Leu
          530          535          540
Lys Asp Ala
545

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<210> SEQ ID NO 78
<211> LENGTH: 527
<212> TYPE: PRT
<213> ORGANISM: Pichia pastoris
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (23)..(37)
<223> OTHER INFORMATION: Variable amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (366)..(378)
<223> OTHER INFORMATION: Variable amino acid
<400> SEQUENCE: 78

```

Ser	Phe	Glu	Asn	Ser	Pro	Val	Phe	Asp	Phe	Leu	Ser	Pro	Phe	Gly	Pro
1				5					10					15	
Ala	Pro	Asn	Gln	Trp	Val	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		20						25					30		
Xaa	Xaa	Xaa	Xaa	Xaa	Val	Gly	Leu	Gly	Ser	Tyr	Ser	Gly	Phe	Asn	Thr
		35					40					45			
Pro	Pro	Met	Tyr	Gly	Asp	Phe	Glu	Ala	Gln	Arg	His	Trp	Met	Glu	Ile
	50					55					60				
Thr	Gln	His	Leu	Ser	Ile	Glu	Lys	Trp	Tyr	Phe	Tyr	Asp	Leu	Gln	Tyr
65					70					75					80
Trp	Gly	Leu	Asp	Tyr	Pro	Pro	Leu	Thr	Ala	Phe	His	Ser	Tyr	Phe	Phe
			85						90					95	
Gly	Lys	Leu	Gly	Ser	Phe	Ile	Asn	Pro	Ala	Trp	Phe	Ala	Leu	Asp	Val
			100					105					110		
Ser	Arg	Gly	Phe	Glu	Ser	Val	Asp	Leu	Lys	Ser	Tyr	Met	Arg	Ala	Thr
		115					120					125			
Ala	Ile	Leu	Ser	Glu	Leu	Leu	Cys	Phe	Ile	Pro	Ala	Val	Ile	Trp	Tyr
	130					135					140				
Cys	Arg	Trp	Met	Gly	Leu	Asn	Tyr	Phe	Asn	Gln	Asn	Ala	Ile	Glu	Gln
145					150					155					160
Thr	Ile	Ile	Ala	Ser	Ala	Ile	Leu	Phe	Asn	Pro	Ser	Leu	Ile	Ile	Ile
			165						170					175	
Asp	His	Gly	His	Phe	Gln	Tyr	Asn	Ser	Val	Met	Leu	Gly	Phe	Ala	Leu
			180					185					190		
Leu	Ser	Ile	Leu	Asn	Leu	Leu	Tyr	Asp	Asn	Phe	Ala	Leu	Ala	Ala	Ile
		195					200					205			
Phe	Phe	Val	Leu	Ser	Ile	Ser	Phe	Lys	Gln	Met	Ala	Leu	Tyr	Tyr	Ser
	210					215					220				
Pro	Ile	Met	Phe	Phe	Tyr	Met	Leu	Ser	Val	Ser	Cys	Trp	Pro	Leu	Lys
225					230					235					240
Asn	Phe	Asn	Leu	Leu	Arg	Leu	Ala	Thr	Ile	Ser	Ile	Ala	Val	Leu	Leu
			245						250					255	
Thr	Phe	Ala	Thr	Leu	Leu	Leu	Pro	Phe	Val	Leu	Val	Asp	Gly	Met	Ser
			260					265					270		
Gln	Ile	Gly	Gln	Ile	Leu	Phe	Arg	Val	Phe	Pro	Phe	Ser	Arg	Gly	Leu
		275					280					285			
Phe	Glu	Asp	Lys	Val	Ala	Asn	Phe	Trp	Cys	Thr	Thr	Asn	Ile	Leu	Val
	290					295					300				
Lys	Tyr	Lys	Gln	Leu	Phe	Thr	Asp	Lys	Thr	Leu	Thr	Arg	Ile	Ser	Leu
305					310					315					320
Val	Ala	Thr	Leu	Ile	Ala	Ile	Ser	Pro	Ser	Cys	Phe	Ile	Ile	Phe	Thr
			325						330					335	
His	Pro	Lys	Lys	Val	Leu	Leu	Pro	Trp	Ala	Phe	Ala	Ala	Cys	Ser	Trp
			340					345					350		
Ala	Phe	Tyr	Leu	Phe	Ser	Phe	Gln	Val	His	Glu	Lys	Ser	Xaa	Xaa	Xaa
		355					360					365			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Lys	Asp	Leu	Asp	Ile
	370					375					380				
Ile	Ser	Met	Val	Cys	Trp	Ile	Ser	Asn	Ile	Ala	Phe	Phe	Ser	Met	Trp
385					390					395					400
Pro	Leu	Leu	Lys	Arg	Asp	Gly	Leu	Ala	Leu	Glu	Tyr	Phe	Val	Leu	Gly
			405						410					415	
Ile	Leu	Ser	Asn	Trp	Leu	Ile	Gly	Asn	Leu	Asn	Trp	Ile	Ser	Lys	Trp
			420					425					430		
Leu	Val	Pro	Ser	Phe	Leu	Ile	Pro	Gly	Pro	Thr	Leu	Ser	Lys	Lys	Val

<400> SEQUENCE: 79

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Val Lys Tyr Lys Glu Arg Phe Thr Ile Gln Gln Leu Gln Leu Tyr Ser
305          310          315          320
Leu Ile Ala Thr Val Ile Gly Phe Leu Pro Ala Met Ile Met Thr Leu
          325          330          335
Leu His Pro Lys Lys His Leu Leu Pro Tyr Val Leu Ile Ala Cys Ser
          340          345          350
Met Ser Phe Phe Leu Phe Ser Phe Gln Val His Glu Lys Thr Ile Leu
          355          360          365
Ile Pro Leu Leu Pro Ile Thr Leu Leu Tyr Ser Ser Thr Asp Trp Asn
          370          375          380
Val Leu Ser Leu Val Ser Trp Ile Asn Asn Val Ala Leu Phe Thr Leu
385          390          395          400
Trp Pro Leu Leu Lys Lys Asp Gly Leu His Leu Gln Tyr Ala Val Ser
          405          410          415
Phe Leu Leu Ser Asn Trp Leu Ile Gly Asn Phe Ser Phe Ile Thr Pro
          420          425          430
Arg Phe Leu Pro Lys Ser Leu Thr Pro Gly Pro Ser Ile Ser Ser Ile
          435          440          445
Asn Ser Asp Tyr Arg Arg Arg Ser Leu Leu Pro Tyr Asn Val Val Trp
          450          455          460
Lys Ser Phe Ile Ile Gly Thr Tyr Ile Ala Met Gly Phe Tyr His Phe
465          470          475          480
Leu Asp Gln Phe Val Ala Pro Pro Ser Lys Tyr Pro Asp Leu Trp Val
          485          490          495
Leu Leu Asn Cys Ala Val Gly Phe Ile Cys Phe Ser Ile Phe Trp Leu
          500          505          510
Trp Ser Tyr Tyr Lys Ile Phe Thr Ser Gly Ser Lys Ser Met Lys Asp
          515          520          525

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<210> SEQ ID NO 80
<211> LENGTH: 511
<212> TYPE: PRT
<213> ORGANISM: Pichia pastoris
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (22)..(36)
<223> OTHER INFORMATION: Variable amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (365)..(379)
<223> OTHER INFORMATION: Variable amino acid
<400> SEQUENCE: 80

```

```

Phe Glu Asn Ser Pro Val Phe Asp Phe Leu Ser Pro Phe Gly Pro Ala
 1          5          10          15
Pro Asn Gln Trp Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
          20          25          30
Xaa Xaa Xaa Xaa Val Gly Leu Gly Ser Tyr Ser Gly Phe Asn Thr Pro
          35          40          45
Pro Met Tyr Gly Asp Phe Glu Ala Gln Arg His Trp Met Glu Ile Thr
          50          55          60
Gln His Leu Ser Ile Glu Lys Trp Tyr Phe Tyr Asp Leu Gln Tyr Trp
          65          70          75          80
Gly Leu Asp Tyr Pro Pro Leu Thr Ala Phe His Ser Tyr Phe Phe Gly
          85          90          95
Lys Leu Gly Ser Phe Ile Asn Pro Ala Trp Phe Ala Leu Asp Val Ser

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<210> SEQ ID NO 81
<211> LENGTH: 480
<212> TYPE: PRT
```

<213> ORGANISM: Schizosaccharomyces pombe

<400> SEQUENCE: 81

```

Phe Glu Asn Gly Ala Pro Val Gln Gln Phe Val Ser Arg Phe Arg Ser
 1          5          10          15
Tyr Ser Ser Lys Phe Leu Phe Phe Pro Cys Leu Ile Met Ser Leu Val
          20          25          30
Phe Met Gln Trp Leu Ile Ser Ile Gly Pro Tyr Ser Gly Tyr Asn Thr
          35          40          45
Pro Pro Met Tyr Gly Asp Phe Glu Ala Gln Arg His Trp Met Glu Leu
          50          55          60
Thr Leu His Thr Pro Val Ser Gln Trp Tyr Phe Arg Asp Leu Gln Trp
          65          70          75          80
Trp Gly Leu Asp Tyr Pro Pro Leu Thr Ala Tyr Val Ser Trp Phe Phe
          85          90          95
Gly Ile Ile Gly His Tyr Phe Phe Asn Pro Glu Trp Phe Ala Asp Val
          100          105          110
Thr Ser Arg Gly Phe Glu Ser Leu Glu Leu Lys Leu Phe Met Arg Ser
          115          120          125
Thr Val Ile Ala Ser His Leu Leu Ile Leu Val Pro Pro Leu Met Phe
          130          135          140
Tyr Ser Lys Trp Trp Ser Arg Arg Ile Pro Asn Phe Val Asp Arg Asn
          145          150          155          160
Ala Ser Leu Ile Met Val Leu Phe Gln Pro Ala Leu Leu Leu Ile Asp
          165          170          175
His Gly His Phe Gln Tyr Asn Cys Val Met Leu Gly Leu Val Met Tyr
          180          185          190
Ala Ile Ala Asn Leu Leu Lys Asn Gln Tyr Val Ala Ala Thr Phe Phe
          195          200          205
Phe Cys Leu Ala Leu Thr Phe Lys Gln Met Ala Leu Tyr Phe Ala Pro
          210          215          220
Pro Ile Phe Phe Tyr Leu Leu Gly Thr Cys Val Lys Pro Lys Ile Arg
          225          230          235          240
Phe Ser Arg Phe Ile Leu Leu Ser Val Thr Val Val Phe Thr Phe Ser
          245          250          255
Leu Ile Leu Phe Pro Trp Ile Tyr Met Asp Tyr Lys Thr Leu Leu Pro
          260          265          270
Gln Ile Leu His Arg Val Phe Pro Phe Ala Arg Gly Leu Trp Glu Asp
          275          280          285
Lys Val Ala Asn Phe Trp Cys Thr Leu Asn Thr Val Phe Lys Ile Arg
          290          295          300
Glu Val Phe Thr Leu His Gln Leu Gln Val Ile Ser Leu Ile Phe Thr
          305          310          315          320
Leu Ile Ser Ile Leu Pro Ser Cys Val Ile Leu Phe Leu Tyr Pro Arg
          325          330          335
Lys Arg Leu Leu Ala Leu Gly Phe Ala Ser Ala Ser Trp Gly Phe Phe
          340          345          350
Leu Phe Ser Phe Gln Val His Glu Lys Ser Val Leu Leu Pro Leu Leu
          355          360          365
Pro Thr Ser Ile Leu Leu Cys His Gly Asn Ile Thr Thr Lys Pro Trp
          370          375          380
Ile Ala Leu Ala Asn Asn Leu Ala Val Phe Ser Leu Trp Pro Leu Leu
          385          390          395          400
Lys Lys Asp Gly Leu Gly Leu Gln Tyr Phe Thr Leu Val Leu Met Trp
          405          410          415
Asn Trp Ile Gly Asp Met Val Val Phe Ser Lys Asn Val Leu Phe Arg

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          420          425          430
Phe Ile Gln Leu Ser Phe Tyr Val Gly Met Ile Val Ile Leu Gly Ile
          435          440          445
Asp Leu Phe Ile Pro Pro Pro Ser Arg Tyr Pro Asp Leu Trp Val Ile
          450          455          460
Leu Asn Val Thr Leu Ser Phe Ala Gly Phe Phe Thr Ile Tyr Leu Trp
          465          470          475          480

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<210> SEQ ID NO 82
<211> LENGTH: 477
<212> TYPE: PRT
<213> ORGANISM: Pichia pastoris
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (329)..(341)
<223> OTHER INFORMATION: Variable amino acid
<400> SEQUENCE: 82

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```

Val Gly Leu Gly Ser Tyr Ser Gly Phe Asn Thr Pro Pro Met Tyr Gly
  1          5          10          15
Asp Phe Glu Ala Gln Arg His Trp Met Glu Ile Thr Gln His Leu Ser
          20          25          30
Ile Glu Lys Trp Tyr Phe Tyr Asp Leu Gln Tyr Trp Gly Leu Asp Tyr
          35          40          45
Pro Pro Leu Thr Ala Phe His Ser Tyr Phe Phe Gly Lys Leu Gly Ser
          50          55          60
Phe Ile Asn Pro Ala Trp Phe Ala Leu Asp Val Ser Arg Gly Phe Glu
          65          70          75          80
Ser Val Asp Leu Lys Ser Tyr Met Arg Ala Thr Ala Ile Leu Ser Glu
          85          90          95
Leu Leu Cys Phe Ile Pro Ala Val Ile Trp Tyr Cys Arg Trp Met Gly
          100          105          110
Leu Asn Tyr Phe Asn Gln Asn Ala Ile Glu Gln Thr Ile Ile Ala Ser
          115          120          125
Ala Ile Leu Phe Asn Pro Ser Leu Ile Ile Ile Asp His Gly His Phe
          130          135          140
Gln Tyr Asn Ser Val Met Leu Gly Phe Ala Leu Leu Ser Ile Leu Asn
          145          150          155          160
Leu Leu Tyr Asp Asn Phe Ala Leu Ala Ala Ile Phe Phe Val Leu Ser
          165          170          175
Ile Ser Phe Lys Gln Met Ala Leu Tyr Tyr Ser Pro Ile Met Phe Phe
          180          185          190
Tyr Met Leu Ser Val Ser Cys Trp Pro Leu Lys Asn Phe Asn Leu Leu
          195          200          205
Arg Leu Ala Thr Ile Ser Ile Ala Val Leu Leu Thr Phe Ala Thr Leu
          210          215          220
Leu Leu Pro Phe Val Leu Val Asp Gly Met Ser Gln Ile Gly Gln Ile
          225          230          235          240
Leu Phe Arg Val Phe Pro Phe Ser Arg Gly Leu Phe Glu Asp Lys Val
          245          250          255
Ala Asn Phe Trp Cys Thr Thr Asn Ile Leu Val Lys Tyr Lys Gln Leu
          260          265          270
Phe Thr Asp Lys Thr Leu Thr Arg Ile Ser Leu Val Ala Thr Leu Ile
          275          280          285
Ala Ile Ser Pro Ser Cys Phe Ile Ile Phe Thr His Pro Lys Lys Val
          290          295          300

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Leu Leu Pro Trp Ala Phe Ala Ala Cys Ser Trp Ala Phe Tyr Leu Phe
305          310          315          320
Ser Phe Gln Val His Glu Lys Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa
          325          330          335
Xaa Xaa Xaa Xaa Xaa Glu Lys Asp Leu Asp Ile Ile Ser Met Val Cys
          340          345          350
Trp Ile Ser Asn Ile Ala Phe Phe Ser Met Trp Pro Leu Lys Arg
          355          360          365
Asp Gly Leu Ala Leu Glu Tyr Phe Val Leu Gly Ile Leu Ser Asn Trp
370          375          380
Leu Ile Gly Asn Leu Asn Trp Ile Ser Lys Trp Leu Val Pro Ser Phe
385          390          395          400
Leu Ile Pro Gly Pro Thr Leu Ser Lys Lys Val Pro Lys Arg Asp Thr
          405          410          415
Lys Thr Val Val His Thr His Trp Phe Trp Gly Ser Val Thr Phe Val
          420          425          430
Ser Tyr Leu Gly Ala Thr Val Ile Gln Phe Val Asp Trp Leu Tyr Leu
          435          440          445
Pro Pro Ala Lys Tyr Pro Asp Leu Trp Val Ile Leu Asn Thr Thr Leu
          450          455          460
Ser Phe Ala Cys Phe Gly Leu Phe Trp Leu Trp Ile Asn
465          470          475

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<210> SEQ ID NO 83

<211> LENGTH: 448

<212> TYPE: PRT

<213> ORGANISM: *Drosophila melanogaster*

<400> SEQUENCE: 83

```

Ile Ser Leu Tyr Ser Tyr Ser Gly Phe Asp Ser Pro Pro Met His Gly
 1          5          10          15
Asp Tyr Glu Ala Gln Arg His Trp Gln Glu Ile Thr Val Asn Leu Ala
          20          25          30
Val Gly Glu Trp Tyr Thr Asn Ser Ser Asn Asn Asp Leu Gln Tyr Trp
          35          40          45
Gly Leu Asp Tyr Pro Pro Leu Thr Ala Tyr His Ser Tyr Leu Val Gly
          50          55          60
Arg Ile Gly Ala Ser Ile Asp Pro Arg Phe Val Glu Leu His Lys Ser
          65          70          75          80
Arg Gly Phe Glu Ser Lys Glu His Lys Arg Phe Met Arg Ala Thr Val
          85          90          95
Val Ser Ala Asp Val Leu Ile Tyr Leu Pro Ala Met Leu Leu Leu Ala
          100          105          110
Tyr Ser Leu Asp Lys Ala Phe Arg Ser Asp Asp Lys Leu Phe Leu Phe
          115          120          125
Thr Leu Val Ala Ala Tyr Pro Gly Gln Thr Leu Ile Asp Asn Gly His
          130          135          140
Phe Gln Tyr Asn Asn Ile Ser Leu Gly Phe Ala Ala Val Ala Ile Ala
145          150          155          160
Ala Ile Leu Arg Arg Arg Phe Tyr Ala Ala Ala Phe Phe Phe Thr Leu
          165          170          175
Ala Leu Asn Tyr Lys Gln Met Glu Leu Tyr His Ser Leu Pro Phe Phe
          180          185          190
Ala Phe Leu Leu Gly Glu Cys Val Ser Gln Lys Ser Phe Ala Ser Phe
          195          200          205
Ile Ala Glu Ile Ser Arg Ile Ala Ala Val Val Leu Gly Thr Phe Ala

```

210		215		220
Ile Leu Trp Val Pro Trp Leu Gly Ser Leu Gln Ala Val Leu Gln Val				
225		230		235
Leu His Arg Leu Phe Pro Val Ala Arg Gly Val Phe Glu Asp Lys Val				240
	245		250	255
Ala Asn Val Trp Cys Ala Val Asn Val Val Trp Lys Leu Lys Lys His				
	260		265	270
Ile Ser Asn Asp Gln Met Ala Leu Val Cys Ile Ala Cys Thr Leu Ile				
	275		280	285
Ala Ser Leu Pro Thr Asn Val Leu Leu Phe Arg Arg Arg Thr Asn Val				
	290		295	300
Gly Phe Leu Leu Ala Leu Phe Asn Thr Ser Leu Ala Phe Phe Leu Phe				
305		310		315
Ser Phe Gln Val His Glu Lys Thr Ile Leu Leu Thr Ala Leu Pro Ala				
	325		330	335
Leu Phe Leu Leu Lys Cys Trp Pro Asp Glu Met Ile Leu Phe Leu Glu				
	340		345	350
Val Thr Val Phe Ser Met Leu Pro Leu Leu Ala Arg Asp Glu Leu Leu				
	355		360	365
Val Pro Ala Val Val Ala Thr Val Ala Phe His Leu Ile Phe Lys Cys				
	370		375	380
Phe Asp Ser Lys Ser Lys Leu Ser Asn Glu Tyr Pro Leu Lys Tyr Ile				
385		390		395
Ala Asn Ile Ser Gln Ile Leu Met Ile Ser Val Val Val Ala Ser Leu				
	405		410	415
Thr Val Pro Ala Pro Thr Lys Tyr Pro Asp Leu Trp Pro Leu Ile Ile				
	420		425	430
Ser Val Thr Ser Cys Gly His Phe Phe Leu Phe Phe Leu Trp Gly Asn				
	435		440	445

<210> SEQ ID NO 84
 <211> LENGTH: 478
 <212> TYPE: PRT
 <213> ORGANISM: Pichia pastoris
 <220> FEATURE:
 <221> NAME/KEY: MOD_RES
 <222> LOCATION: (324)..(336)
 <223> OTHER INFORMATION: Variable amino acid
 <400> SEQUENCE: 84

Tyr Ser Gly Phe Asn Thr Pro Pro Met Tyr Gly Asp Phe Glu Ala Gln				
1		5		10
Arg His Trp Met Glu Ile Thr Gln His Leu Ser Ile Glu Lys Trp Tyr				
	20		25	30
Phe Tyr Asp Leu Gln Tyr Trp Gly Leu Asp Tyr Pro Pro Leu Thr Ala				
	35		40	45
Phe His Ser Tyr Phe Phe Gly Lys Leu Gly Ser Phe Ile Asn Pro Ala				
	50		55	60
Trp Phe Ala Leu Asp Val Ser Arg Gly Phe Glu Ser Val Asp Leu Lys				
	65		70	75
Ser Tyr Met Arg Ala Thr Ala Ile Leu Ser Glu Leu Leu Cys Phe Ile				
	85		90	95
Pro Ala Val Ile Trp Tyr Cys Arg Trp Met Gly Leu Asn Tyr Phe Asn				
	100		105	110
Gln Asn Ala Ile Glu Gln Thr Ile Ile Ala Ser Ala Ile Leu Phe Asn				
	115		120	125

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Pro Ser Leu Ile Ile Ile Asp His Gly His Phe Gln Tyr Asn Ser Val
 130          135          140
Met Leu Gly Phe Ala Leu Leu Ser Ile Leu Asn Leu Leu Tyr Asp Asn
145          150          155          160
Phe Ala Leu Ala Ala Ile Phe Phe Val Leu Ser Ile Ser Phe Lys Gln
          165          170          175
Met Ala Leu Tyr Tyr Ser Pro Ile Met Phe Phe Tyr Met Leu Ser Val
          180          185          190
Ser Cys Trp Pro Leu Lys Asn Phe Asn Leu Leu Arg Leu Ala Thr Ile
          195          200          205
Ser Ile Ala Val Leu Leu Thr Phe Ala Thr Leu Leu Leu Pro Phe Val
          210          215          220
Leu Val Asp Gly Met Ser Gln Ile Gly Gln Ile Leu Phe Arg Val Phe
225          230          235          240
Pro Phe Ser Arg Gly Leu Phe Glu Asp Lys Val Ala Asn Phe Trp Cys
          245          250          255
Thr Thr Asn Ile Leu Val Lys Tyr Lys Gln Leu Phe Thr Asp Lys Thr
          260          265          270
Leu Thr Arg Ile Ser Leu Val Ala Thr Leu Ile Ala Ile Ser Pro Ser
          275          280          285
Cys Phe Ile Ile Phe Thr His Pro Lys Lys Val Leu Leu Pro Trp Ala
          290          295          300
Phe Ala Ala Cys Ser Trp Ala Phe Tyr Leu Phe Ser Phe Gln Val His
305          310          315          320
Glu Lys Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
          325          330          335
Glu Lys Asp Leu Asp Ile Ile Ser Met Val Cys Trp Ile Ser Asn Ile
          340          345          350
Ala Phe Phe Ser Met Trp Pro Leu Leu Lys Arg Asp Gly Leu Ala Leu
          355          360          365
Glu Tyr Phe Val Leu Gly Ile Leu Ser Asn Trp Leu Ile Gly Asn Leu
          370          375          380
Asn Trp Ile Ser Lys Trp Leu Val Pro Ser Phe Leu Ile Pro Gly Pro
385          390          395          400
Thr Leu Ser Lys Lys Val Pro Lys Arg Asp Thr Lys Thr Val Val His
          405          410          415
Thr His Trp Phe Trp Gly Ser Val Thr Phe Val Ser Tyr Leu Gly Ala
          420          425          430
Thr Val Ile Gln Phe Val Asp Trp Leu Tyr Leu Pro Pro Ala Lys Tyr
          435          440          445
Pro Asp Leu Trp Val Ile Leu Asn Thr Thr Leu Ser Phe Ala Cys Phe
          450          455          460
Gly Leu Phe Trp Leu Trp Ile Asn Tyr Asn Leu Tyr Ile Leu
465          470          475

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<210> SEQ ID NO 85

<211> LENGTH: 459

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 85

```

Tyr Ser Gly Ala Gly Ile Pro Pro Lys Phe Gly Asp Phe Glu Ala Gln
 1          5          10          15
Arg His Trp Met Glu Ile Thr Thr Asn Leu Pro Val Ile Asp Trp Tyr
          20          25          30
Arg Asn Gly Thr Tyr Asn Asp Leu Thr Tyr Trp Gly Leu Asp Tyr Pro

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<211> LENGTH: 836

<212> TYPE: DNA

<213> ORGANISM: Kluyveromyces lactis

<400> SEQUENCE: 86

```

atctctgttt caacagctct tgcattcatt ggttctttcg gtccaatcta tatctttgga 60
ggatacaaga acttagtgca atcaatgcac aggatttttc catttgccag gggatatctt 120
gaagataaag ttgcgaattt ttggtgcgtt tctaataatt tcatcaaata tagaaatcta 180
ttcactcaga aggatcttca attatactca ttactcgcaa cagttattgg gcttttacca 240
tcattcatta taacattttt ataccggaag agacatttac taccatatgc tttggccgca 300
tggtcgatgt cattcttctt attcagcttc caggttcatg aaaagacaat cttattacct 360
ttacttccta ttacactctt gtacacgtca agagattgga atgttctatc attggtttgt 420
tggattaaca acgtggcatt gtttacactc tggccattac tgaaaaagga caatctagta 480
ttgcaatatg gagtcatgtt catgttttagc aattggttga tcggttaactt cagtttcgtc 540
acaccacgct tcctcccaaa atttttgaca ccagggccat ccatcagtga tatagatgtt 600
gattatagac gggcaagttt actacccaag agcctaatat ggagattaat cattgttggc 660
tcatatattg caatggggat tattcatttt ctagactatt acgtctcccc gccatcaaaa 720
taccctgatt tatgggtgct tgccaattgt tccttgggct tctcatgttt tgtgacattt 780
tggatatgga acaattataa ttattcgaaa tgagaaacag cactttgcaa gattta 836

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<210> SEQ ID NO 87

<211> LENGTH: 277

<212> TYPE: PRT

<213> ORGANISM: Kluyveromyces lactis

<400> SEQUENCE: 87

```

Ile Ser Val Ser Thr Ala Leu Ala Phe Ile Gly Ser Phe Gly Pro Ile
 1           5           10           15
Tyr Ile Phe Gly Gly Tyr Lys Asn Leu Val Gln Ser Met His Arg Ile
          20           25           30
Phe Pro Phe Ala Arg Gly Ile Phe Glu Asp Lys Val Ala Asn Phe Trp
          35           40           45
Cys Val Ser Asn Ile Phe Ile Lys Tyr Arg Asn Leu Phe Thr Gln Lys
          50           55           60
Asp Leu Gln Leu Tyr Ser Leu Leu Ala Thr Val Ile Gly Leu Leu Pro
          65           70           75           80
Ser Phe Ile Ile Thr Phe Leu Tyr Pro Lys Arg His Leu Leu Pro Tyr
          85           90           95
Ala Leu Ala Ala Cys Ser Met Ser Phe Phe Leu Phe Ser Phe Gln Val
          100          105          110
His Glu Lys Thr Ile Leu Leu Pro Leu Leu Pro Ile Thr Leu Leu Tyr
          115          120          125
Thr Ser Arg Asp Trp Asn Val Leu Ser Leu Val Cys Trp Ile Asn Asn
          130          135          140
Val Ala Leu Phe Thr Leu Trp Pro Leu Leu Lys Lys Asp Asn Leu Val
          145          150          155          160
Leu Gln Tyr Gly Val Met Phe Met Phe Ser Asn Trp Leu Ile Gly Asn
          165          170          175
Phe Ser Phe Val Thr Pro Arg Phe Leu Pro Lys Phe Leu Thr Pro Gly
          180          185          190
Pro Ser Ile Ser Asp Ile Asp Val Asp Tyr Arg Arg Ala Ser Leu Leu
          195          200          205
Pro Lys Ser Leu Ile Trp Arg Leu Ile Ile Val Gly Ser Tyr Ile Ala
          210          215          220
Met Gly Ile Ile His Phe Leu Asp Tyr Tyr Val Ser Pro Pro Ser Lys
          225          230          235          240
Tyr Pro Asp Leu Trp Val Leu Ala Asn Cys Ser Leu Gly Phe Ser Cys

```



```

                245                250                255
Phe Val Thr Phe Trp Ile Trp Asn Asn Tyr Asn Tyr Ser Lys Glu Thr
                260                265                270
Ala Leu Cys Lys Ile
                275

```

```

<210> SEQ ID NO 88
<211> LENGTH: 284
<212> TYPE: PRT
<213> ORGANISM: Kluyveromyces lactis
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (116)..(127)
<223> OTHER INFORMATION: Variable amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (271)
<223> OTHER INFORMATION: Variable amino acid
<400> SEQUENCE: 88

```

```

Ile Ser Val Ser Thr Ala Leu Ala Phe Ile Gly Ser Phe Gly Pro Ile
 1          5          10          15
Tyr Ile Phe Gly Gly Tyr Lys Asn Leu Val Gln Ser Met His Arg Ile
          20          25          30
Phe Pro Phe Ala Arg Gly Ile Phe Glu Asp Lys Val Ala Asn Phe Trp
          35          40          45
Cys Val Ser Asn Ile Phe Ile Lys Tyr Arg Asn Leu Phe Thr Gln Lys
          50          55          60
Asp Leu Gln Leu Tyr Ser Leu Leu Ala Thr Val Ile Gly Leu Leu Pro
          65          70          75          80
Ser Phe Ile Ile Thr Phe Leu Tyr Pro Lys Arg His Leu Leu Pro Tyr
          85          90          95
Ala Leu Ala Ala Cys Ser Met Ser Phe Phe Leu Phe Ser Phe Gln Val
          100          105          110
His Glu Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr
          115          120          125
Thr Ser Arg Asp Trp Asn Val Leu Ser Leu Val Cys Trp Ile Asn Asn
          130          135          140
Val Ala Leu Phe Thr Leu Trp Pro Leu Leu Lys Lys Asp Asn Leu Val
          145          150          155          160
Leu Gln Tyr Gly Val Met Phe Met Phe Ser Asn Trp Leu Ile Gly Asn
          165          170          175
Phe Ser Phe Val Thr Pro Arg Phe Leu Pro Lys Phe Leu Thr Pro Gly
          180          185          190
Pro Ser Ile Ser Asp Ile Asp Val Asp Tyr Arg Arg Ala Ser Leu Leu
          195          200          205
Pro Lys Ser Leu Ile Trp Arg Leu Ile Ile Val Gly Ser Tyr Ile Ala
          210          215          220
Met Gly Ile Ile His Phe Leu Asp Tyr Tyr Val Ser Pro Pro Ser Gln
          225          230          235          240
Glu Arg Tyr Lys Tyr Pro Asp Leu Trp Val Leu Ala Asn Cys Ser Leu
          245          250          255
Gly Phe Ser Cys Phe Val Thr Phe Trp Ile Trp Asn Asn Tyr Xaa Leu
          260          265          270
Phe Glu Arg Met Arg Asn Ser Thr Leu Gln Asp Leu
          275          280

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<210> SEQ ID NO 89
<211> LENGTH: 280
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces cerevisiae
<400> SEQUENCE: 89
Ile Ala Phe Ala Thr Leu Ala Thr Phe Ala Ile Ile Phe Ala Pro Leu
 1           5           10           15
Tyr Phe Leu Gly Gly Leu Lys Asn Ile His Gln Cys Ile His Arg
           20           25           30
Ile Phe Pro Phe Ala Arg Gly Ile Phe Glu Asp Lys Val Ala Asn Phe
           35           40           45
Trp Cys Val Thr Asn Val Phe Val Lys Tyr Lys Glu Arg Phe Thr Ile
           50           55           60
Gln Gln Leu Gln Leu Tyr Ser Leu Ile Ala Thr Val Ile Gly Phe Leu
           65           70           75           80
Pro Ala Met Ile Met Thr Leu Leu His Pro Lys Lys His Leu Leu Pro
           85           90           95
Tyr Val Leu Ile Ala Cys Ser Met Ser Phe Phe Leu Phe Ser Phe Gln
           100          105          110
Val His Glu Lys Thr Ile Leu Ile Pro Leu Leu Pro Ile Thr Leu Leu
           115          120          125
Tyr Ser Ser Thr Asp Trp Asn Val Leu Ser Leu Val Ser Trp Ile Asn
           130          135          140
Asn Val Ala Leu Phe Thr Leu Trp Pro Leu Leu Lys Lys Asp Gly Leu
           145          150          155          160
His Leu Gln Tyr Ala Val Ser Phe Leu Leu Ser Asn Trp Leu Ile Gly
           165          170          175
Asn Phe Ser Phe Ile Thr Pro Arg Phe Leu Pro Lys Ser Leu Thr Pro
           180          185          190
Gly Pro Ser Ile Ser Ser Ile Asn Ser Asp Tyr Arg Arg Arg Ser Leu
           195          200          205
Leu Pro Tyr Asn Val Val Trp Lys Ser Phe Ile Ile Gly Thr Tyr Ile
           210          215          220
Ala Met Gly Phe Tyr His Phe Leu Asp Gln Phe Val Ala Pro Pro Ser
           225          230          235          240
Lys Tyr Pro Asp Leu Trp Val Leu Leu Asn Cys Ala Val Gly Phe Ile
           245          250          255
Cys Phe Ser Ile Phe Trp Leu Trp Ser Tyr Tyr Lys Ile Phe Thr Ser
           260          265          270
Gly Ser Lys Ser Met Lys Asp Leu
           275          280

```

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<210> SEQ ID NO 90
<211> LENGTH: 284
<212> TYPE: PRT
<213> ORGANISM: Kluyveromyces lactis
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (116)..(127)
<223> OTHER INFORMATION: Variable amino acid
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (271)
<223> OTHER INFORMATION: Variable amino acid

```

<400> SEQUENCE: 90

```

Ile Ser Val Ser Thr Ala Leu Ala Phe Ile Gly Ser Phe Gly Pro Ile
 1           5           10           15
Tyr Ile Phe Gly Gly Tyr Lys Asn Leu Val Gln Ser Met His Arg Ile
          20           25           30
Phe Pro Phe Ala Arg Gly Ile Phe Glu Asp Lys Val Ala Asn Phe Trp
          35           40           45
Cys Val Ser Asn Ile Phe Ile Lys Tyr Arg Asn Leu Phe Thr Gln Lys
          50           55           60
Asp Leu Gln Leu Tyr Ser Leu Leu Ala Thr Val Ile Gly Leu Leu Pro
          65           70           75           80
Ser Phe Ile Ile Thr Phe Leu Tyr Pro Lys Arg His Leu Leu Pro Tyr
          85           90           95
Ala Leu Ala Ala Cys Ser Met Ser Phe Phe Leu Phe Ser Phe Gln Val
          100           105           110
His Glu Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr
          115           120           125
Thr Ser Arg Asp Trp Asn Val Leu Ser Leu Val Cys Trp Ile Asn Asn
          130           135           140
Val Ala Leu Phe Thr Leu Trp Pro Leu Leu Lys Lys Asp Asn Leu Val
          145           150           155           160
Leu Gln Tyr Gly Val Met Phe Met Phe Ser Asn Trp Leu Ile Gly Asn
          165           170           175
Phe Ser Phe Val Thr Pro Arg Phe Leu Pro Lys Phe Leu Thr Pro Gly
          180           185           190
Pro Ser Ile Ser Asp Ile Asp Val Asp Tyr Arg Arg Ala Ser Leu Leu
          195           200           205
Pro Lys Ser Leu Ile Trp Arg Leu Ile Ile Val Gly Ser Tyr Ile Ala
          210           215           220
Met Gly Ile Ile His Phe Leu Asp Tyr Tyr Val Ser Pro Pro Ser Gln
          225           230           235           240
Glu Arg Tyr Lys Tyr Pro Asp Leu Trp Val Leu Ala Asn Cys Ser Leu
          245           250           255
Gly Phe Ser Cys Phe Val Thr Phe Trp Ile Trp Asn Asn Tyr Xaa Leu
          260           265           270
Phe Glu Arg Met Arg Asn Ser Thr Leu Gln Asp Leu
          275           280

```

<210> SEQ ID NO 91

<211> LENGTH: 250

<212> TYPE: PRT

<213> ORGANISM: Schizosaccharomyces pombe

<400> SEQUENCE: 91

```

Leu Ser Val Thr Val Val Phe Thr Phe Ser Leu Ile Leu Phe Pro Trp
 1           5           10           15
Ile Tyr Met Asp Tyr Lys Thr Leu Leu Pro Gln Ile Leu His Arg Val
          20           25           30
Phe Pro Phe Ala Arg Gly Leu Trp Glu Asp Lys Val Ala Asn Phe Trp
          35           40           45
Cys Thr Leu Asn Thr Val Phe Lys Ile Arg Glu Val Phe Thr Leu His
          50           55           60
Gln Leu Gln Val Ile Ser Leu Ile Phe Thr Leu Ile Ser Ile Leu Pro
          65           70           75           80
Ser Cys Val Ile Leu Phe Leu Tyr Pro Arg Lys Arg Leu Leu Ala Leu
          85           90           95

```

```

Gly Phe Ala Ser Ala Ser Trp Gly Phe Phe Leu Phe Ser Phe Gln Val
      100      105      110
His Glu Lys Ser Val Leu Leu Pro Leu Leu Pro Thr Ser Ile Leu Leu
      115      120      125
Cys His Gly Asn Ile Thr Thr Lys Pro Trp Ile Ala Leu Ala Asn Asn
      130      135      140
Leu Ala Val Phe Ser Leu Trp Pro Leu Leu Lys Lys Asp Gly Leu Gly
145      150      155      160
Leu Gln Tyr Phe Thr Leu Val Leu Met Trp Asn Trp Ile Gly Asp Met
      165      170      175
Val Val Phe Ser Lys Asn Val Leu Phe Arg Phe Ile Gln Leu Ser Phe
      180      185      190
Tyr Val Gly Met Ile Val Ile Leu Gly Ile Asp Leu Phe Ile Pro Pro
      195      200      205
Pro Ser Arg Tyr Pro Asp Leu Trp Val Ile Leu Asn Val Thr Leu Ser
      210      215      220
Phe Ala Gly Phe Phe Thr Ile Tyr Leu Trp Thr Leu Gly Arg Leu Leu
225      230      235      240
His Ile Ser Ser Lys Leu Ser Thr Asp Leu
      245      250

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<210> SEQ ID NO 92
<211> LENGTH: 238
<212> TYPE: PRT
<213> ORGANISM: Kluyveromyces lactis
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (88)..(99)
<223> OTHER INFORMATION: Variable amino acid
<400> SEQUENCE: 92

```

```

Met His Arg Ile Phe Pro Phe Ala Arg Gly Ile Phe Glu Asp Lys Val
  1      5      10      15
Ala Asn Phe Trp Cys Val Ser Asn Ile Phe Ile Lys Tyr Arg Asn Leu
      20      25      30
Phe Thr Gln Lys Asp Leu Gln Leu Tyr Ser Leu Leu Ala Thr Val Ile
      35      40      45
Gly Leu Leu Pro Ser Phe Ile Ile Thr Phe Leu Tyr Pro Lys Arg His
      50      55      60
Leu Leu Pro Tyr Ala Leu Ala Ala Cys Ser Met Ser Phe Phe Leu Phe
      65      70      75      80
Ser Phe Gln Val His Glu Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      85      90      95
Xaa Xaa Xaa Tyr Thr Ser Arg Asp Trp Asn Val Leu Ser Leu Val Cys
      100      105      110
Trp Ile Asn Asn Val Ala Leu Phe Thr Leu Trp Pro Leu Leu Lys Lys
      115      120      125
Asp Asn Leu Val Leu Gln Tyr Gly Val Met Phe Met Phe Ser Asn Trp
      130      135      140
Leu Ile Gly Asn Phe Ser Phe Val Thr Pro Arg Phe Leu Pro Lys Phe
145      150      155      160
Leu Thr Pro Gly Pro Ser Ile Ser Asp Ile Asp Val Asp Tyr Arg Arg
      165      170      175
Ala Ser Leu Leu Pro Lys Ser Leu Ile Trp Arg Leu Ile Ile Val Gly
      180      185      190
Ser Tyr Ile Ala Met Gly Ile Ile His Phe Leu Asp Tyr Tyr Val Ser

```

```

          195                200                205
Pro Pro Ser Lys Tyr Pro Asp Leu Trp Val Leu Ala Asn Cys Ser Leu
      210                215                220
Gly Phe Ser Cys Phe Val Thr Phe Trp Ile Trp Asn Asn Tyr
225                230                235

```

<210> SEQ ID NO 93

<211> LENGTH: 219

<212> TYPE: PRT

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 93

```

Leu Ser Arg Leu Ala Pro Phe Glu Arg Gly Ile Tyr Glu Asp Tyr Val
 1                5                10                15
Ala Asn Phe Trp Cys Thr Thr Ser Ile Leu Ile Lys Trp Lys Asn Leu
      20                25                30
Phe Thr Thr Gln Ser Leu Lys Ser Ile Ser Leu Ala Ala Thr Ile Leu
      35                40                45
Ala Ser Leu Pro Ser Met Val Gln Gln Ile Leu Ser Pro Ser Asn Glu
      50                55                60
Gly Phe Leu Tyr Gly Leu Leu Asn Ser Ser Met Ala Phe Tyr Leu Phe
      65                70                75                80
Ser Phe Gln Val His Glu Lys Ser Ile Leu Met Pro Phe Leu Ser Ala
      85                90                95
Thr Leu Leu Ala Leu Lys Leu Pro Asp His Phe Ser His Leu Thr Tyr
      100                105                110
Tyr Ala Leu Phe Ser Met Phe Pro Leu Leu Cys Arg Asp Lys Leu Leu
      115                120                125
Ile Pro Tyr Leu Thr Leu Ser Phe Leu Phe Thr Val Ile Tyr His Ser
      130                135                140
Pro Gly Asn His His Ala Ile Gln Lys Thr Asp Val Ser Phe Phe Ser
      145                150                155                160
Phe Lys Asn Phe Pro Gly Tyr Val Phe Leu Leu Arg Thr His Phe Phe
      165                170                175
Ile Ser Val Val Leu His Val Leu Tyr Leu Thr Ile Lys Pro Pro Gln
      180                185                190
Lys Tyr Pro Phe Leu Phe Glu Ala Leu Ile Met Ile Leu Cys Phe Ser
      195                200                205
Tyr Phe Ile Met Phe Ala Phe Tyr Thr Asn Tyr
      210                215

```

<210> SEQ ID NO 94

<211> LENGTH: 252

<212> TYPE: PRT

<213> ORGANISM: Kluyveromyces lactis

<220> FEATURE:

<221> NAME/KEY: MOD_RES

<222> LOCATION: (114)..(125)

<223> OTHER INFORMATION: Variable amino acid

<400> SEQUENCE: 94

```

Val Ser Thr Ala Leu Ala Phe Ile Gly Ser Phe Gly Pro Ile Tyr Ile
 1                5                10                15
Phe Gly Gly Tyr Lys Asn Leu Val Gln Ser Met His Arg Ile Phe Pro
      20                25                30
Phe Ala Arg Gly Ile Phe Glu Asp Lys Val Ala Asn Phe Trp Cys Val
      35                40                45

```

```

Ser Asn Ile Phe Ile Lys Tyr Arg Asn Leu Phe Thr Gln Lys Asp Leu
  50          55          60
Gln Leu Tyr Ser Leu Leu Ala Thr Val Ile Gly Leu Leu Pro Ser Phe
  65          70          75          80
Ile Ile Thr Phe Leu Tyr Pro Lys Arg His Leu Leu Pro Tyr Ala Leu
          85          90          95
Ala Ala Cys Ser Met Ser Phe Phe Leu Phe Ser Phe Gln Val His Glu
          100          105          110
Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Thr Ser
          115          120          125
Arg Asp Trp Asn Val Leu Ser Leu Val Cys Trp Ile Asn Asn Val Ala
          130          135          140
Leu Phe Thr Leu Trp Pro Leu Leu Lys Lys Asp Asn Leu Val Leu Gln
          145          150          155          160
Tyr Gly Val Met Phe Met Val Thr Pro Arg Phe Leu Pro Lys Phe Leu
          165          170          175
Thr Pro Gly Pro Ser Ile Ser Asp Ile Asp Val Asp Tyr Arg Arg Ala
          180          185          190
Ser Leu Leu Pro Lys Ser Leu Ile Trp Arg Leu Ile Ile Val Gly Ser
          195          200          205
Tyr Ile Ala Met Gly Ile Ile His Phe Leu Asp Tyr Tyr Val Ser Pro
          210          215          220
Pro Ser Lys Tyr Pro Asp Leu Trp Val Leu Ala Asn Cys Ser Leu Gly
          225          230          235          240
Phe Ser Cys Phe Val Thr Phe Trp Ile Trp Asn Asn
          245          250

```

<210> SEQ ID NO 95

<211> LENGTH: 259

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 95

```

Val Lys Leu Ala Cys Ile Val Val Ala Ser Phe Val Leu Cys Trp Leu
  1          5          10          15
Pro Phe Phe Thr Glu Arg Glu Gln Thr Leu Gln Val Leu Arg Arg Leu
          20          25          30
Phe Pro Val Asp Arg Gly Leu Phe Glu Asp Lys Val Ala Asn Ile Trp
          35          40          45
Cys Ser Phe Asn Val Phe Leu Lys Ile Lys Asp Ile Leu Pro Arg His
          50          55          60
Ile Gln Leu Ile Met Ser Phe Cys Phe Thr Phe Leu Ser Leu Leu Pro
          65          70          75          80
Ala Cys Ile Lys Leu Ile Leu Gln Pro Ser Ser Lys Gly Phe Lys Phe
          85          90          95
Thr Leu Val Ser Cys Ala Leu Ser Phe Phe Leu Phe Ser Phe Gln Val
          100          105          110
His Glu Lys Ser Ile Leu Leu Val Ser Leu Pro Val Cys Leu Val Leu
          115          120          125
Ser Glu Ile Pro Phe Met Ser Thr Trp Phe Leu Leu Val Ser Thr Phe
          130          135          140
Ser Met Leu Pro Leu Leu Leu Lys Asp Glu Leu Leu Met Pro Ser Val
          145          150          155          160
Val Thr Thr Met Ala Phe Phe Ile Ala Cys Val Thr Ser Phe Ser Ile
          165          170          175
Phe Glu Lys Thr Ser Glu Glu Glu Leu Gln Leu Lys Ser Phe Ser Ile

```

	180		185		190										
Ser	Val	Arg	Lys	Tyr	Leu	Pro	Cys	Phe	Thr	Phe	Leu	Ser	Arg	Ile	Ile
	195		200		205										
Gln	Tyr	Leu	Phe	Leu	Ile	Ser	Val	Ile	Thr	Met	Val	Leu	Leu	Thr	Leu
	210		215		220										
Met	Thr	Val	Thr	Leu	Asp	Pro	Pro	Gln	Lys	Leu	Pro	Asp	Leu	Phe	Ser
	225		230		235										
Val	Leu	Val	Cys	Phe	Val	Ser	Cys	Leu	Asn	Phe	Leu	Phe	Phe	Leu	Val
			245						250					255	
Tyr	Phe	Asn													

<210> SEQ ID NO 96

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 96

```

atgaagatga gacgctacaa gctctttctc atgttctgta tggctggcct gtgcctcata 60
tccttcctgc acttctttaa gaccttatcc tatgtcacct tcccgagaga actggcctcc 120
ctcagcccta acctcgtatc cagcttcttc tggacaatg cccctgtcac tcccaggcc 180
agtccggagc cgggtggccc cgacctattg cggacacccc tctactccca ctctccctg 240
ctccagccac tgtccccgag caaggccaca gaggaactgc accgggtgga cttcgtgttg 300
ccggaggaca ccacggagta ttttgtgcgc accaaagctg gtggtgtgtg cttcaaacca 360
ggtaccagga tgctggagaa accttcgcca gggcgagacag aggagaagcc cgaagtgtct 420
gagggctcct cagcccgggg acctgctcgg agggccatga ggcacgtgtt gagtacgcgg 480
gagcgccctg gcagccgggg cactaggcgc aagtgggttg agtgtgtgtg cctgccaggc 540
tggcacgggc ccagttgcgg ggtgccacg gtggtgcagt attccaacct gccaccaag 600
gaacgcctg taccaggga ggtaccgagg cgggttatca acgccatcaa catcaaccac 660
gagttcgacc tgctggatgt gcgcttccat gagctgggag atgttggtga cgccttcgtg 720
gtctgtgaat ctaatttcac cgcctacggg gagcctcggc cgctcaagtt ccgagagatg 780
ctgaccaatg gcaccttcga gtacatccgc cacaaggtgc tctatgtctt cctggaccat 840
tccccacctg gtggccgtca ggacggctgg attgcggatg actacctgcg caccttcctc 900
accaggatg gcgtctccc cctgcgcaac ctgcggccc atgacgtctt tatcatcgac 960
gatgcggacg agatccctgc gcgtgatggt gtgctgttcc tcaaactcta cgatggctgg

1020 acagagccct tcgccttcca catgcggaag tccctgtatg gtttcttctg gaagcagccg
1080 ggcacactgg aggtggtgtc aggctgcacc atggacatgc tgcaggccgt gtatgggctg
1140 gatggcatcc gcctgcgccc ccgccagtac tacaccatgc ccaacttccg gcagtatgag
1200 aaccgcaccg gccacatcct agtgcagtgg tctctcggca gccccctgca cttcgcgggc
1260 tggcattgct cctggtgctt cacaccgag ggcattctact ttaaactcgt gtcagcccag
1320 aatggcgact tccccgctg gggtgactat gaggacaaga gggacctcaa ttacatccgc
1380 agcttgatcc gcactggggg atggttcgac ggaacgcagc aggagtaccc tctgcggac
1440 cccagtgagc acatgtatgc tcctaaatac ctgctcaaga actatgacca gttccgctac
1500 ttgctggaaa atccctaccg ggagcccaag agcactgtag agggtgggcg ccagaaccag
1560 ggctcagatg gaaggccatc tgctgtcagg ggcaagttgg atacagtgga gggctag
1617

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<210> SEQ ID NO 97

<211> LENGTH: 536

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 97

```

Met Arg Arg Tyr Lys Leu Phe Leu Met Phe Cys Met Ala Gly Leu Cys
 1           5           10           15
Leu Ile Ser Phe Leu His Phe Phe Lys Thr Leu Ser Tyr Val Thr Phe
           20           25           30
Pro Arg Glu Leu Ala Ser Leu Ser Pro Asn Leu Ile Ser Ser Phe Phe
           35           40           45
Trp Asn Asn Ala Pro Val Thr Pro Gln Ala Ser Pro Glu Pro Gly Asp
           50           55           60
Pro Asp Leu Leu Arg Thr Pro Leu Tyr Ser His Ser Pro Leu Leu Gln
           65           70           75           80
Pro Leu Ser Pro Ser Lys Ala Thr Glu Glu Leu His Arg Val Asp Phe
           85           90           95
Val Leu Pro Glu Asp Thr Thr Glu Tyr Phe Val Arg Thr Lys Ala Gly
           100          105          110
Gly Val Cys Phe Lys Pro Gly Thr Arg Met Leu Glu Lys Pro Ser Pro
           115          120          125
Gly Arg Thr Glu Glu Lys Thr Glu Val Ser Glu Gly Ser Ser Ala Arg
           130          135          140
Gly Pro Ala Arg Arg Pro Met Arg His Val Leu Ser Ser Arg Glu Arg
           145          150          155          160
Leu Gly Ser Arg Gly Thr Arg Arg Lys Trp Val Glu Cys Val Cys Leu
           165          170          175
Pro Gly Trp His Gly Pro Ser Cys Gly Val Pro Thr Val Val Gln Tyr
           180          185          190
Ser Asn Leu Pro Thr Lys Glu Arg Leu Val Pro Arg Glu Val Pro Arg
           195          200          205
Arg Val Ile Asn Ala Ile Asn Ile Asn His Glu Phe Asp Leu Leu Asp
           210          215          220
Val Arg Phe His Glu Leu Gly Asp Val Val Asp Ala Phe Val Val Cys
           225          230          235          240
Asp Ser Asn Phe Thr Ala Tyr Gly Glu Pro Arg Pro Leu Lys Phe Arg
           245          250          255
Glu Met Leu Thr Asn Gly Thr Phe Glu Tyr Ile Arg His Lys Val Leu
           260          265          270
Tyr Val Phe Leu Asp His Phe Pro Pro Gly Gly Arg Gln Asp Gly Trp
           275          280          285
Ile Ala Asp Asp Tyr Leu Arg Thr Phe Leu Thr Gln Asp Gly Val Ser
           290          295          300
Arg Leu Arg Asn Leu Arg Pro Asp Asp Val Phe Ile Ile Asp Asp Ala
           305          310          315          320
Asp Glu Ile Pro Ala Arg Asp Gly Val Leu Phe Leu Lys Leu Tyr Asp
           325          330          335
Gly Trp Thr Glu Pro Phe Ala Phe His Met Arg Lys Ser Leu Tyr Gly
           340          345          350
Phe Phe Trp Lys Gln Pro Gly Thr Leu Glu Val Val Ser Gly Cys Thr
           355          360          365
Met Asp Met Leu Gln Ala Val Tyr Gly Leu Asp Gly Ile Arg Leu Arg
           370          375          380
Arg Arg Gln Tyr Tyr Thr Met Pro Asn Phe Arg Gln Tyr Glu Asn Arg
           385          390          395          400

```


Thr	Gly	His	Ile	Leu	Val	Gln	Trp	Ser	Leu	Gly	Ser	Pro	Leu	His	Phe
				405					410					415	
Ala	Gly	Trp	His	Cys	Ser	Trp	Cys	Phe	Thr	Pro	Glu	Gly	Ile	Tyr	Phe
			420					425					430		
Lys	Leu	Val	Ser	Ala	Gln	Asn	Gly	Asp	Phe	Pro	Arg	Trp	Gly	Asp	Tyr
		435					440					445			
Glu	Asp	Lys	Arg	Asp	Leu	Asn	Tyr	Ile	Arg	Ser	Leu	Ile	Arg	Thr	Gly
	450					455					460				
Gly	Trp	Phe	Asp	Gly	Thr	Gln	Gln	Glu	Tyr	Pro	Pro	Ala	Asp	Pro	Ser
465					470					475					480
Glu	His	Met	Tyr	Ala	Pro	Lys	Tyr	Leu	Leu	Lys	Asn	Tyr	Asp	Gln	Phe
				485				490						495	
Arg	Tyr	Leu	Leu	Glu	Asn	Pro	Tyr	Arg	Glu	Pro	Lys	Ser	Thr	Val	Glu
			500					505					510		
Gly	Gly	Arg	Gln	Asn	Gln	Gly	Ser	Asp	Gly	Arg	Ser	Ser	Ala	Val	Arg
		515					520					525			
Gly	Lys	Leu	Asp	Thr	Ala	Glu	Gly								
	530					535									

<210> SEQ ID NO 98

<211> LENGTH: 2115

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 98

```

gaaatgaacc tctcttattg attttttattg gcctagagcc aggagtactg cattcagttg 60
acttttcaggg taaaaagaaa acagtcctgg ttgtttgtcat cataaacata tggaccagtg 120
tgatggtgaa atgagatgag gctccgcaat ggaactgtag ccaactgcttt agcattttatc 180
acttccttcc ttactttgtc ttggtatact acatggcaaa atgggaaaga aaaactgatt 240
gcttatcaac gagaattcct tgctttgaaa gaacgtcttc gaatagctga acacagaatc 300
tcacagcgct cttctgaatt aaatacgatt gtgcaacagt tcaagcgtgt aggagcagaa 360
acaaatggaa gtaaggatgc gttgaataag ttttcagata ataccctaaa gctgttaaag 420
gagttaacaa gcaaaaaatc tcttcaagtg ccaagtattt attatcattt gcctcattta 480
ttgaaaaatg aaggaagtct tcaacctgct gtacagattg gcaacggaag aacaggagtt 540
tcaatagtca tgggcattcc cacagtgaag agagaagtta aatcttacct catagaaact 600
cttcattccc ttattgataa cctgtatcct gaagagaagt tggactgtgt tatagtagtc 660
ttcataggag agacagatat tgattatgta catggtgttg tagccaacct ggagaaagaa 720
ttttctaaag aaatcagttc tggcttggtg gaagtcatat cacccttga aagctattat 780
cctgacttga caaacctaaa ggagacattt ggagactcca aagaaagagt aagatggaga 840
acaaagcaaa acctagatta ctgttttcta atgatgtatg ctcaagaaaa gggcatatat 900
tacattcagc ttgaagatga tattattgtc aaacaaaatt attttaatac cataaaaaat 960
tttgcacttc aactttcttc tgaggaatgg atgattctag agttttccca gctgggcttc

1020 attggtaaaa tgtttcaagc gccggatctt actctgattg tagaattcat attcatgttt
1080 tacaaggaga aaccattga ttggctcctg gaccatattc tctgggtgaa agtctgcaac
1140 cctgaaaaag atgcaaaaca ttgtgataga cagaaagcaa atctgcgaat tcgcttcaga
1200 ccttcccttt tccaacatgt tggctctgcac tcatcactat caggaaaaat ccaaaaactc
1260 acggataaag attatatgaa accattactt cttaaaatcc atgtaaaccc acctgcggag
1320 gtatctactt ccttgaaggc ctaccaaggg catacgctgg agaaaactta catgggagag
1380

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1440 gattttcttct gggctatcac accgatagct ggagactaca tcttgtttaa atttgataaa
1500 ccagtcaatg tagaaagtta tttgttccat agcggcaacc aagaacatcc tggagatatt
1560 ctgctaaaca caactgtgga agttttgcct ttttaagagtg aagggtttgga aataagcaaa
1620 gaaaccaaag acaaacgatt agaagatggc tatttcagaa taggaaaatt tgagaatggt
1680 gttgcagaag gaatggtgga tccaagtctc aatcccattt cagcctttcg actttcagtt
1740 attcagaatt ctgctgtttg ggccattctt aatgagattc atattaaaaa agccaccaac
1800 tgatcatctg agaaaccaac acatttttttc ctgtgaattt gttaattaaa gatagttaag
1860 catgtatctt ttttttattt ctacttgaac actacctctt gtgaagtcta ctgtagataa
1920 gacgattgtc atttccactt ggaaagtgaa tctcccataa taattgtatt tgtttgaaac
1980 taagctgtcc tcagatttta acttgactca aacatttttc aattatgaca gcctgttaat
2040 atgacttgta ctatttttgt attatactaa tacataagag ttgtacatat tgttacattc
2100 tttaaatttg agaaaaacta atgttacata cattttatga aggggggtact tttgaggttc
2115 acttattttta ctatt

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<210> SEQ ID NO 99

<211> LENGTH: 535

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 99

```

Met Arg Leu Arg Asn Gly Thr Val Ala Thr Ala Leu Ala Phe Ile Thr
  1           5           10           15
Ser Phe Leu Thr Leu Ser Trp Tyr Thr Trp Gln Asn Gly Lys Glu
          20           25           30
Lys Leu Ile Ala Tyr Gln Arg Glu Phe Leu Ala Leu Lys Glu Arg Leu
          35           40           45
Arg Ile Ala Glu His Arg Ile Ser Gln Arg Ser Ser Glu Leu Asn Thr
          50           55           60
Ile Val Gln Gln Phe Lys Arg Val Gly Ala Glu Thr Asn Gly Ser Lys
          65           70           75           80
Asp Ala Leu Asn Lys Phe Ser Asp Asn Thr Leu Lys Leu Leu Lys Glu
          85           90           95
Leu Thr Ser Lys Lys Ser Leu Gln Val Pro Ser Ile Tyr Tyr His Leu
          100          105          110
Pro His Leu Leu Lys Asn Glu Gly Ser Leu Gln Pro Ala Val Gln Ile
          115          120          125
Gly Asn Gly Arg Thr Gly Val Ser Ile Val Met Gly Ile Pro Thr Val
          130          135          140
Lys Arg Glu Val Lys Ser Tyr Leu Ile Glu Thr Leu His Ser Leu Ile
          145          150          155          160
Asp Asn Leu Tyr Pro Glu Glu Lys Leu Asp Cys Val Ile Val Val Phe
          165          170          175
Ile Gly Glu Thr Asp Ile Asp Tyr Val His Gly Val Val Ala Asn Leu

```

<211> LENGTH: 3226

<213> ORGANISM:

<400> SEQUENCE: 100

attagatagag ag

attgcttagag	agagatggct	ttctttttctc	cttgggaagct	gtctctctcag	aagcttgggt	80
ttttctctggt	gacttttcggc	ttcatctatgg	gcatagtgct	tctgcacttc	accatccagc	120
agcggaactca	ccccgagagc	agctccatgtg	tacggggagca	gataccttgac	ctcagcaaga	180
ggtacatttaa	ggcactggca	gaggagaaca	gggacgtggt	ggatggcccc	tacgctggtg	240

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tcatgacagc ctatgatctg aagaaaacgc tcgccgtctt gctggataac atcctgcagc 300
gcattggcaa gctcgagtca aagggtggaca atctgggtcaa cggcacagga gcgaactcca 360
ccaactccac cacggctgtc cccagcttgg tgctcgcttga gaaaattaat gtggcagata 420
tcattaatgg agttcaggaa aaatgtgtat tgccctctat ggatggctac cccactgctg 480
aggggaaaat caagtggatg aaggacatgt ggcgctcgga cccctgctac gcagactatg 540
gagtggacgg gacctcctgc tcctttttta ttacctcag tgaggttgaa aattggtgtc 600
ctcgtttacc ttggagagca aaaaatccct atgaagaagc tgatcataac tcattggcgg 660
aaatccgtac ggattttaac attctctacg gcatgatgaa gaagcacgag gaggctcgtt 720
ggatgaggct tcggatccgg cgaatggctg acgcgtggat ccaagctatc aagtctctgg 780
cggagaaaca aaaccttgag aagaggaaac ggaagaaaat ccttgttcac ctggggctcc 840
tgaccaagga atcgggcttc aagattgcgg agacagcatt cagcgggtggc cctctgggtg 900
aactcgttca gtggagtgc ttaatcacat ctctgtacct gctgggccat gacatccgga 960
tctcggcctc actggctgag ctcaaggaga taatgaagaa ggttggtgga aaccggtctg

1020 gctgtccaac tgtaggagac agaatcgttg agctgattta tatcgatatt gtgggacttg
1080 ctcaatttaa gaaaacacta gggccatcct gggttcatta ccagtgcattg ctccgggtgc
1140 tagactcctt tggaacagaa cctgagttca atcatgctgag ctatgccag tcaaaaggcc
1200 acaagacccc ctggggaaag tggaatctga acccgagca gttttacacc atgttccttc
1260 ataccccaga caacagcttt ctgggcttcg tggaggagca gcacctgaac tccagcgaca
1320 ttcaccacat caacgagatc aaaaggcaga accagtcctt tgtgtatggc aaagtggata
1380 gtttctggaa gaataagaaa atctacctgg atatcattca cacgtacatg gaagtgcacg
1440 ccactgttta tggctccagt accaagaaca ttcccagtta cgtgaaaaac catggcattc
1500 tcagtggacg tgacctgcag tttcttctcc gggaaaccaa gctgttcggt gggctcggat
1560 tcccttatga aggcccagct cccctggagg ccatcgcgaa tggatgtgct ttctgaacc
1620 ccaagttcaa cctcccaaa agcagcaaaa acacagactt cttcattggc aagccaacac
1680 tgagagagct gacatcccag catccttacg cagaagtctt catcggccgg ccacacgtct
1740 ggactgtgga tctcaataac cgagaggaag tagaagatgc agtaaaagcc atcttaaacc
1800 agaagattga gccgtatatg ccatatgagt tcacatgtga aggcattgctg cagagaatca
1860 acgctttcat tgaaaaacag gacttctgcc atggccaagt gatgtggccg cccctcagcg
1920 cctgcaggt taagctggct gagccagggc agtcctgcaa acaggtgtgc caggagagcc
1980 agctcatctg cgagccatcc ttctttcaac acctcaacaa ggaaaaggac ctgctgaagt
2040 ataaggtgac ctgccaaagc tcagaactgt acaaggacat cctggtgccc tccttctacc
2100 ccaagagcaa gcactgtgtg ttccaagggg acctcctgct cttcagttgt gccggagccc
2160 atcccacaca ccagcggatc tgcccctgcc gggacttcat caagggccaa gtggccctct
2220

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2280 gcaaagactg cctatagcat cgctgccctg aattaactca gacgggaaag acgtggctcc
 2340 actgggcagg gccaaagggc acaaagacat tcagggactc tgaccagagc ctgagatctt
 2400 tgggtccaggg cttgagttta gtaccgctcc agccacagcc agtgcacccc agtttacacc
 2460 aaaaccacaa gggaacaggt tagaacagga acctgggttc tcctcagtgt aaggaatgtc
 2520 ctctctgtct gggagatcga gcgactgtag ggaaaggatc caggcagttg ctccccggaa
 2580 tttttttttt tttttttttt aaagaaggga taaaagtccg gagactcatt caaactgaaa
 2640 acaaaacagg aagaggggaat tgagccaatt gggaaggact ttggggccga tcctaaacca
 2700 attaatttat ttatttgga ggatgggggc gggctcggga gggaggagag gggttgaaca
 2760 gtttcctttt gttcctcact gttaattcgc ccaccttcgg gcccttcttg ttctgcagcg
 2820 ccaagcaggg tgcagagggg ctgtggcttg cttgaggggc cactgtgggg cttcactcct
 2880 ggtcacaggt ggcagcagag aaaagagatg tctataagca gggggatgta gctcagtttg
 2940 tagaatgctt gcatagcata aatgaagtcc tgggttccat cccagcacc acataaatgc
 3000 aggtaagaaa cagagtcagg aggaccaagc attctccttg gctacataac aaaagcaagg
 3060 cctttgtccc catgtcttg ctacaagaga ccctatctca gaaaattgtg ggggggaggg
 3120 ggggggaaat ggccttgaaa acacagccag tcaactgtcac tgcattgccga gaactggtgg
 3180 atcccaggtg tgcttggcag ataacagcta aaaggcacat aaccttggtg gggaaataaa
 3226 tgcctgtggt gtcctgaggg cccaccaag ttccaaaaaa aaaaaa

<210> SEQ ID NO 101

<211> LENGTH: 740

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 101

Met	Ala	Phe	Phe	Ser	Pro	Trp	Lys	Leu	Ser	Ser	Gln	Lys	Leu	Gly	Phe
1				5					10					15	
Phe	Leu	Val	Thr	Phe	Gly	Phe	Ile	Trp	Gly	Met	Met	Leu	Leu	His	Phe
			20					25					30		
Thr	Ile	Gln	Gln	Arg	Thr	Gln	Pro	Glu	Ser	Ser	Ser	Met	Leu	Arg	Glu
		35					40					45			
Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Ile	Lys	Ala	Leu	Ala	Glu	Glu
		50				55					60				
Asn	Arg	Asp	Val	Val	Asp	Gly	Pro	Tyr	Ala	Gly	Val	Met	Thr	Ala	Tyr
		65			70					75				80	
Asp	Leu	Lys	Lys	Thr	Leu	Ala	Val	Leu	Leu	Asp	Asn	Ile	Leu	Gln	Arg
			85						90					95	
Ile	Gly	Lys	Leu	Glu	Ser	Lys	Val	Asp	Asn	Leu	Val	Asn	Gly	Thr	Gly
			100					105					110		
Ala	Asn	Ser	Thr	Asn	Ser	Thr	Thr	Ala	Val	Pro	Ser	Leu	Val	Ser	Leu


```

Ser Gln His Pro Tyr Ala Glu Val Phe Ile Gly Arg Pro His Val Trp
                    565                      570                      575
Thr Val Asp Leu Asn Asn Arg Glu Glu Val Glu Asp Ala Val Lys Ala
                    580                      585                      590
Ile Leu Asn Gln Lys Ile Glu Pro Tyr Met Pro Tyr Glu Phe Thr Cys
                    595                      600                      605
Glu Gly Met Leu Gln Arg Ile Asn Ala Phe Ile Glu Lys Gln Asp Phe
                    610                      615                      620
Cys His Gly Gln Val Met Trp Pro Pro Leu Ser Ala Leu Gln Val Lys
625                      630                      635                      640
Leu Ala Glu Pro Gly Gln Ser Cys Lys Gln Val Cys Gln Glu Ser Gln
                    645                      650                      655
Leu Ile Cys Glu Pro Ser Phe Phe Gln His Leu Asn Lys Glu Lys Asp
                    660                      665                      670
Leu Leu Lys Tyr Lys Val Thr Cys Gln Ser Ser Glu Leu Tyr Lys Asp
                    675                      680                      685
Ile Leu Val Pro Ser Phe Tyr Pro Lys Ser Lys His Cys Val Phe Gln
                    690                      695                      700
Gly Asp Leu Leu Leu Phe Ser Cys Ala Gly Ala His Pro Thr His Gln
705                      710                      715                      720
Arg Ile Cys Pro Cys Arg Asp Phe Ile Lys Gly Gln Val Ala Leu Cys
                    725                      730                      735
Lys Asp Cys Leu
                    740

```

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<210> SEQ ID NO 102
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Illustrative
retention signal peptide
<400> SEQUENCE: 102
Lys Asp Glu Leu
1

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<210> SEQ ID NO 103
<211> LENGTH: 60
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces cerevisiae
<400> SEQUENCE: 103
Ile Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser
1          5          10          15
Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro
20          25          30
Ile Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp
35          40          45
Tyr Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro
50          55          60

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<210> SEQ ID NO 104
<211> LENGTH: 58
<212> TYPE: PRT
<213> ORGANISM: Drosophila virilis
<400> SEQUENCE: 104

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```

Leu Pro Phe Phe Leu Cys Asn Phe Ile Gly Val Ala Cys Ala Arg Ser
 1           5           10           15
Leu His Tyr Gln Phe Tyr Ile Trp Tyr Phe His Ser Leu Pro Tyr Leu
           20           25           30
Val Trp Ser Thr Pro Tyr Ser Leu Gly Val Arg Tyr Leu Ile Leu Gly
           35           40           45
Ile Ile Glu Tyr Cys Trp Asn Thr Tyr Pro
 50           55

```

<210> SEQ ID NO 105

<211> LENGTH: 60

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 105

```

Ile Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser
 1           5           10           15
Arg Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro
           20           25           30
Ile Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp
           35           40           45
Tyr Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro
 50           55           60

```

<210> SEQ ID NO 106

<211> LENGTH: 59

<212> TYPE: PRT

<213> ORGANISM: *Drosophila melanogaster*

<400> SEQUENCE: 106

```

Leu Pro Phe Phe Leu Cys Asn Leu Val Gly Val Ala Cys Ala Ser Arg
 1           5           10           15
Ser Leu His Tyr Gln Phe Tyr Val Trp Tyr Phe His Ser Leu Pro Tyr
           20           25           30
Leu Ala Trp Ser Thr Pro Tyr Ser Leu Gly Val Arg Cys Leu Ile Leu
           35           40           45
Gly Leu Ile Glu Tyr Cys Trp Asn Thr Tyr Pro
 50           55

```